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human	Motif 0	
tez1	AKFLHMLMSVYVVELLSFFVYVTEFTTQKNR	
EST2	ISEIEWLVLGKRSNAKMCCLSDFEKQKQIPAEFIYWLNFIIPILOQFFYITESSDLRNR	
p123	LKDFRWLFISD---IWFTKHNFENLNQLAICFISWLFRLQIPKIIQITFFYCTEISSVT-TREISWMQVET-SAKHFYYFDHEN-IYVLWKLRLWFEDLVVSLIRCCFFVYVTEQQKSYSK	*** **
human	Motif 1	
tez1	LFYRKSVWSKLQSIGIRQHLKRQVLRDVSEAEVRQHREARPALLTSRLRFIPKP--DGL	
EST2	TVYFRKDIWKLICRPFI-TSMKMEAPEKINENNVRMDTQK-TTLP PAVIRLLPKK--NTF	
p123	IVYFRHDTWNKLIITPFIIVEYFKTYLVENNVCRNHNSTLS--NFNHSMRIIPKKSNNEF	
	TYYYRKNINDVIMKMSI-ADLKKETLAEVQEKEVEEWKKS-LGFAPGKLRLLIPKK--TTF	*** **
human	Motif 2	
tez1	RPIVNDYVVGARTFRREKRAERLTSRVKALF-SVLNYERA	
EST2	RLITN-LRKRFLIKMGSNKKMLVSTNQTLRPVASILKHLINESSGIPFNLEVYMKLLTF	
p123	RIIAIPCRGADEEFTIYKENHKNAIQPTQKILEYLRNKRPTSTTKIYSPQIADRIKEF	
	RPIMTFNKKIIVNSDRKTTTKLTNTKLLNSHMLMLTKLN-RMFKDPPFGFAVENYDDVMKKY	* *
human	Motif 3 (A)	
tez1	KKDLLKHRMFGR-KKYFVRIDIKSCYDRIKQDLMFRIVKK-KLKDPEFVIRKYATIHTATS	
EST2	KQRLKKFNNVLPELYFMKFDVKSCYDSIPRMECMRILKD-ALKNENGFFVRSQYFFNTN	
p123	EEFVCKWKQVGQPKLFFATMDIEKCYDSVNREKLSTFLKTTKLLSSDFWIMTAQILKRKN	* * *

FIG. 1

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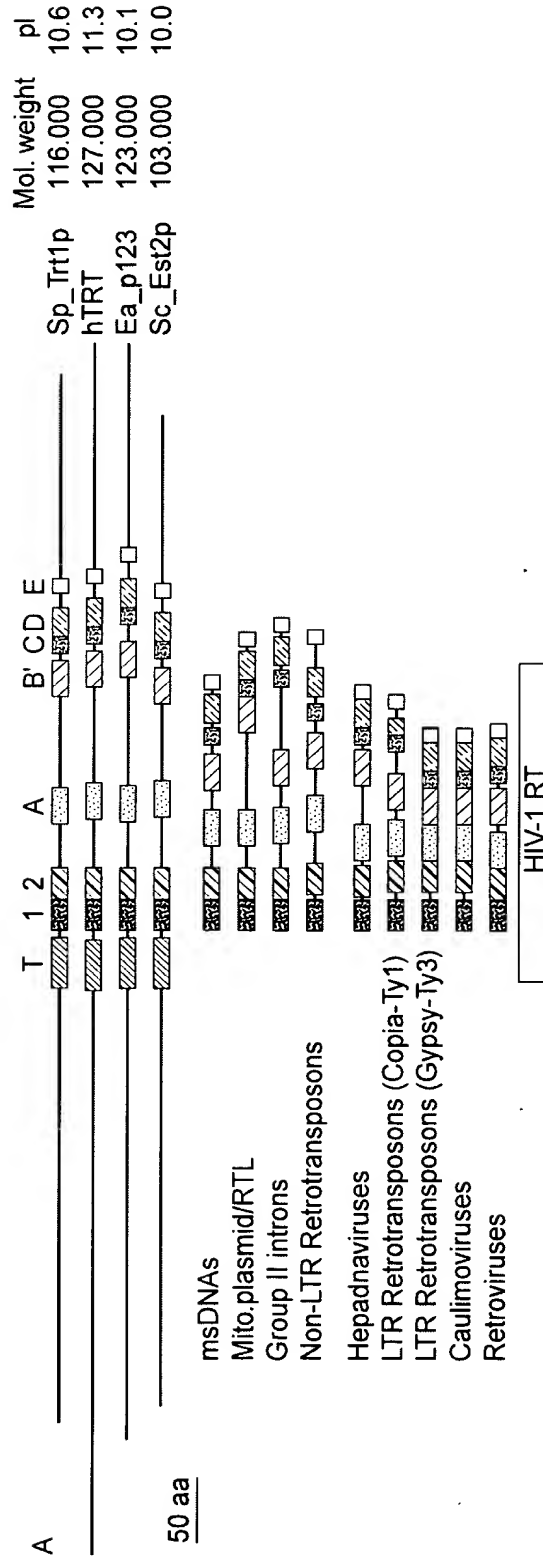


FIG. 2

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3/103



THUMB PALM FINGERS

FIG. 3

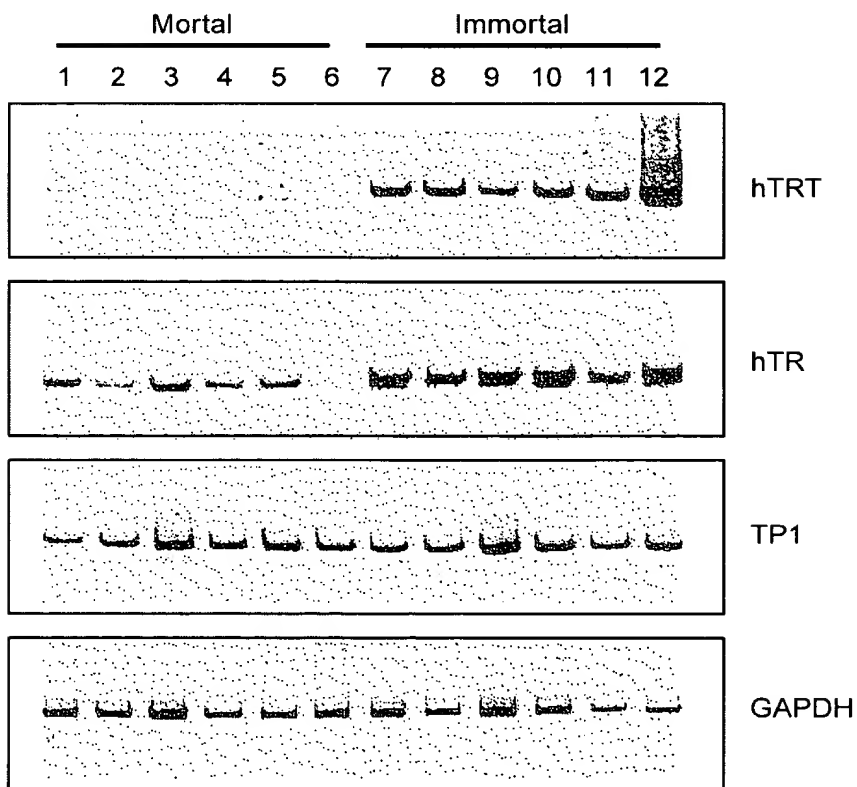


FIG. 5

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TRT con WL hh hh pFFY TE p p Y RK W L h I K
Sp Trt1p 429 WLYNSFIPILOQFFYITESSDLNRNRTVFRKDIWKLCPFITSMKM 8
hTrt 546 WLMSVYVVELLRFFYVTEFTTQKNRFFYRKSVWSKQSIGIRQHLK 10
Ea p123 441 WIFEDLVSLIRCFYVTEQOKSYKTYRKNIDWIMKMSIADLKK 8
Sc_Est2p 366 WLFRLQIPKIIQTFYCYCTEISSTVT-IVYFRHDTWNKLITPFIVEYFK 8

Motif T

TRT con NNVPRMDTQKTTLPPIPAVIRLLPKNT-0 FRhI h h K K
Sp Trt1p EVRQHREARPAALLTSRLRFIPKPDG-0 LRPIVNMVYVVGARTFRREKRAERLTSRV 45
hTrt KEVEWKKSLGFAPGKRLRIPKTT-0 FRPIMTFNKKIVNSDRKTTKLTNTKLLN 41
Ea p123 CRNHNSYTLNHNHSMRRIIPKSN 1 FRIIAIPCRGADEEEETIYKENHKNAIQP 42
Sc_Est2p AF VLPELYFMKF DVKSCYDSIPRMECMRILKDALKN 68

Motif A

Motif 2

Motif 1

RT con LSNELGTKGKFKPMRIVNIPKGG 0 IRPLSVGNPRDKIVQVWMMILDTTFDKK 27
Sc a1 SILRIGYYPDAWKHAQVMILAPGKS 6 YRPISLSSGLSKMFERLLKRLFRVDLFK 32
Dm_TART EGKISKIGPENPYNTPVFAIKKDDST 1 WRKLVDFRELNKRQTQDFWEVOLGIPHPAG 0
HIV-1

Motif B

Motif C

Motif D

Motif E

TRT con K Y Q GIPOGS Ls hL h Y DL F LLRL DDFLhIT A F h G c p N cK W G S
Sp Trt1p SOYLQKVGIPOGSILSSFLCHFYMEDLIDEYLSFT 6 LLRVVDDFLFTVNKD 0 AKKFLNLSLRGFEKHNFTSLEKTVI 17
hTrt KSYVQCQGIPOGSILSTLLCSLCYGDWENKLFAGI 5 LLRLVDDFLFTVPHLTH 0 AKTFLRTLVRGVPEYCVVNLKTVV 19
Ea p123 KFYKQTKGIPOGLCVSSILSSFYATLEESSLGL 14 LMRLLDDYLLITQENN 0 AVLFIEKLINVSRENGFKFNMKLQOT 23
Sc_Est2p KCYIREDEGLFQGSLSAPIVDLVYDDLLLEFYSEFK 8 ILKLADDFLLIISTDQQQ 0 VINIKKLAMGGFQKYNANAKNRDKILA 20

Motif B'

Motif C'

Motif D'

Motif E'

RT con hPOG pP hh h h Y DDhhh Gh h cK h hLG h
Sc a1 TVHKPMLGLPQGSILSPILCNIVMTLVNWNLEDYI 55 YVRYADDDILIGVLGSKN 2 KMKRDLNLFNS-LGLTMNEEKTLI 4
Dm_TART RAGQIGAGVPQGSNLGPILYSIFSSDMPPLPHIYHP 7 LSTYADDDIIVLSSDILA 6 NENYKTFSDWADKMGISVNAAKTGH 25
HIV-1 GIRYQYNVLPQGWKGSIPAIFQSSMTKILEPFFKQN 4 IYQYDDDLVYVGSDEIG 1 HRTKIEELRQHLRLRWGLTTPDKKHQK 0

FIG. 4

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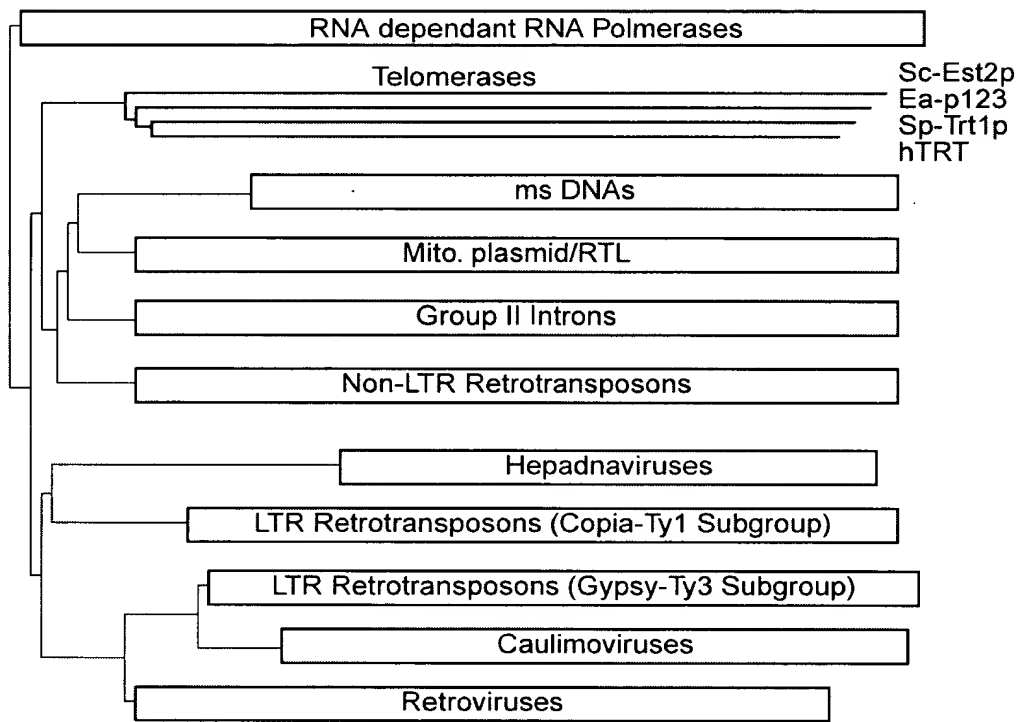


FIG. 6

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6/103

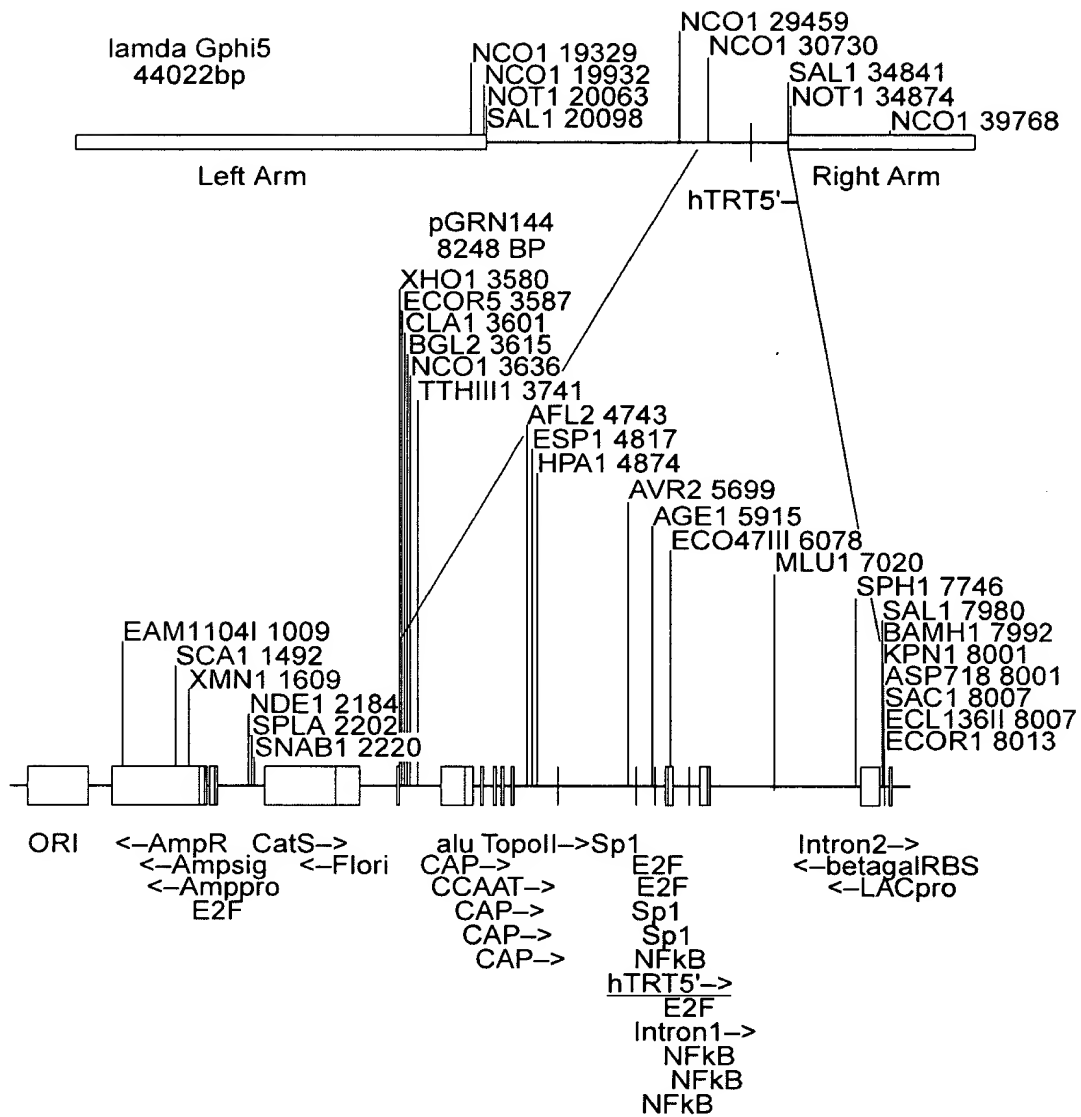


FIG. 7

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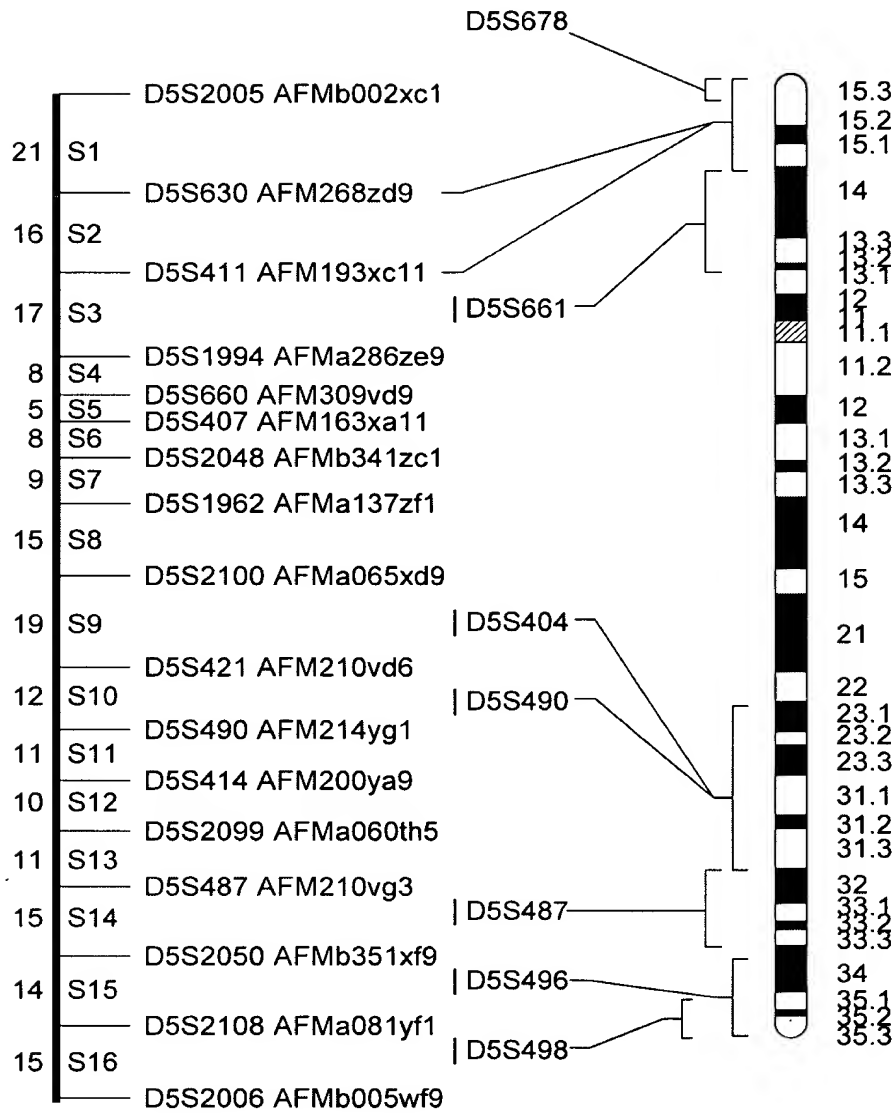
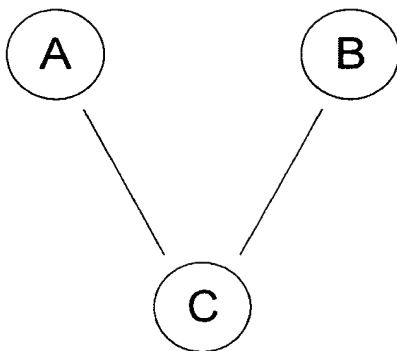


FIG. 8

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8/103



A = pGRN144
 B = pSEAP2-Basic
 C = BGL2-ECO47III fragment from A
 into BGL2-NRU1 sites of B

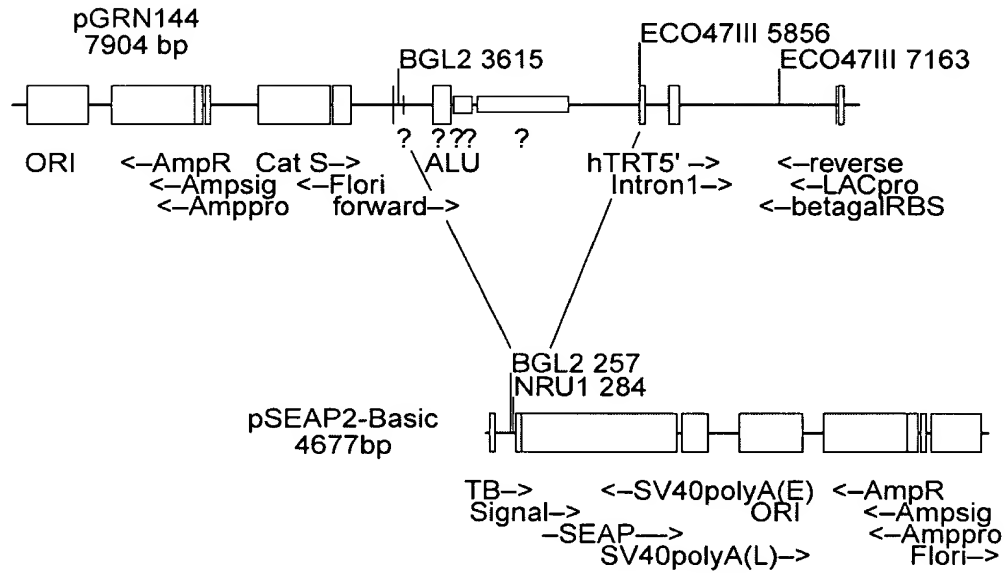


FIG. 9

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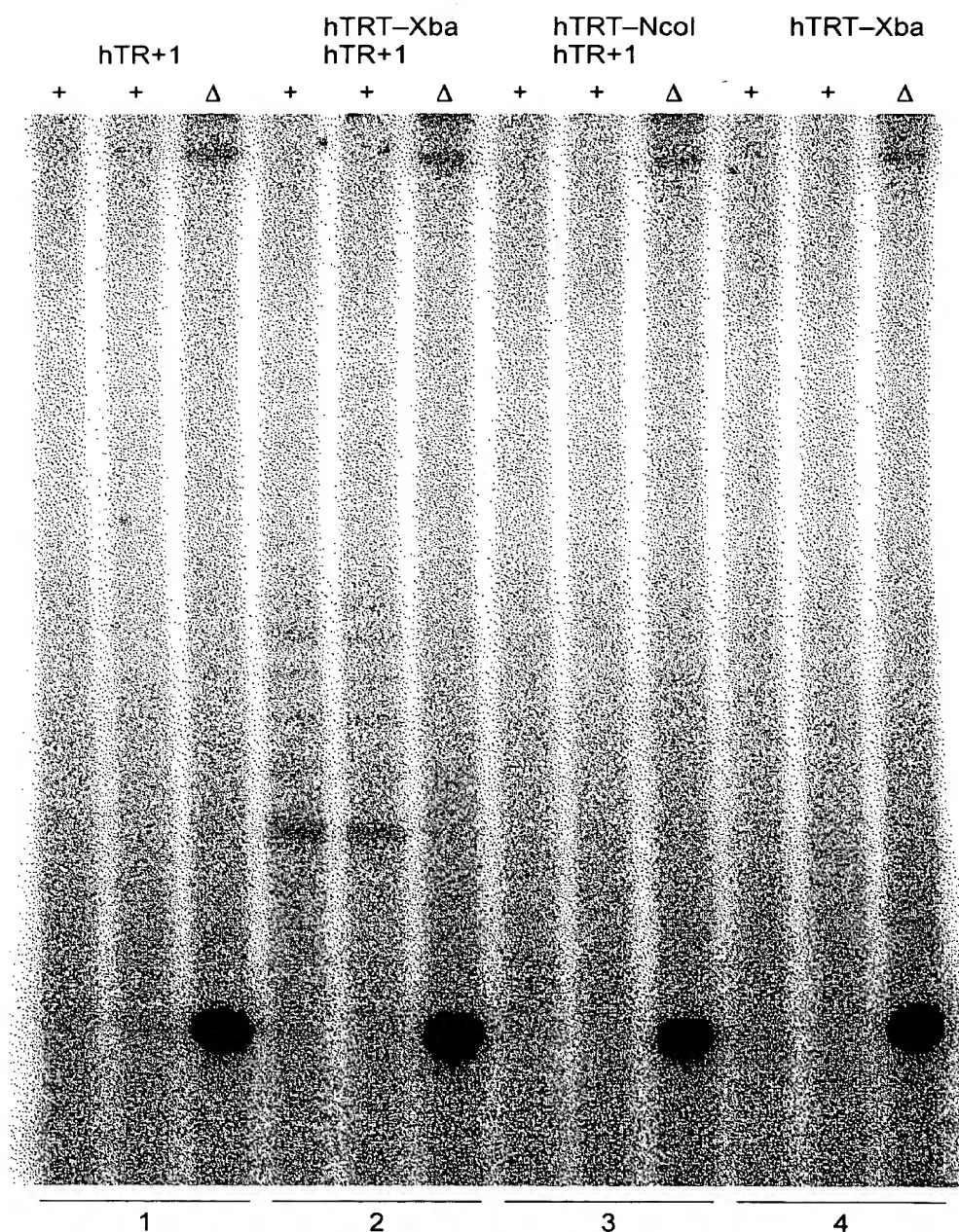


FIG. 10A

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10/103

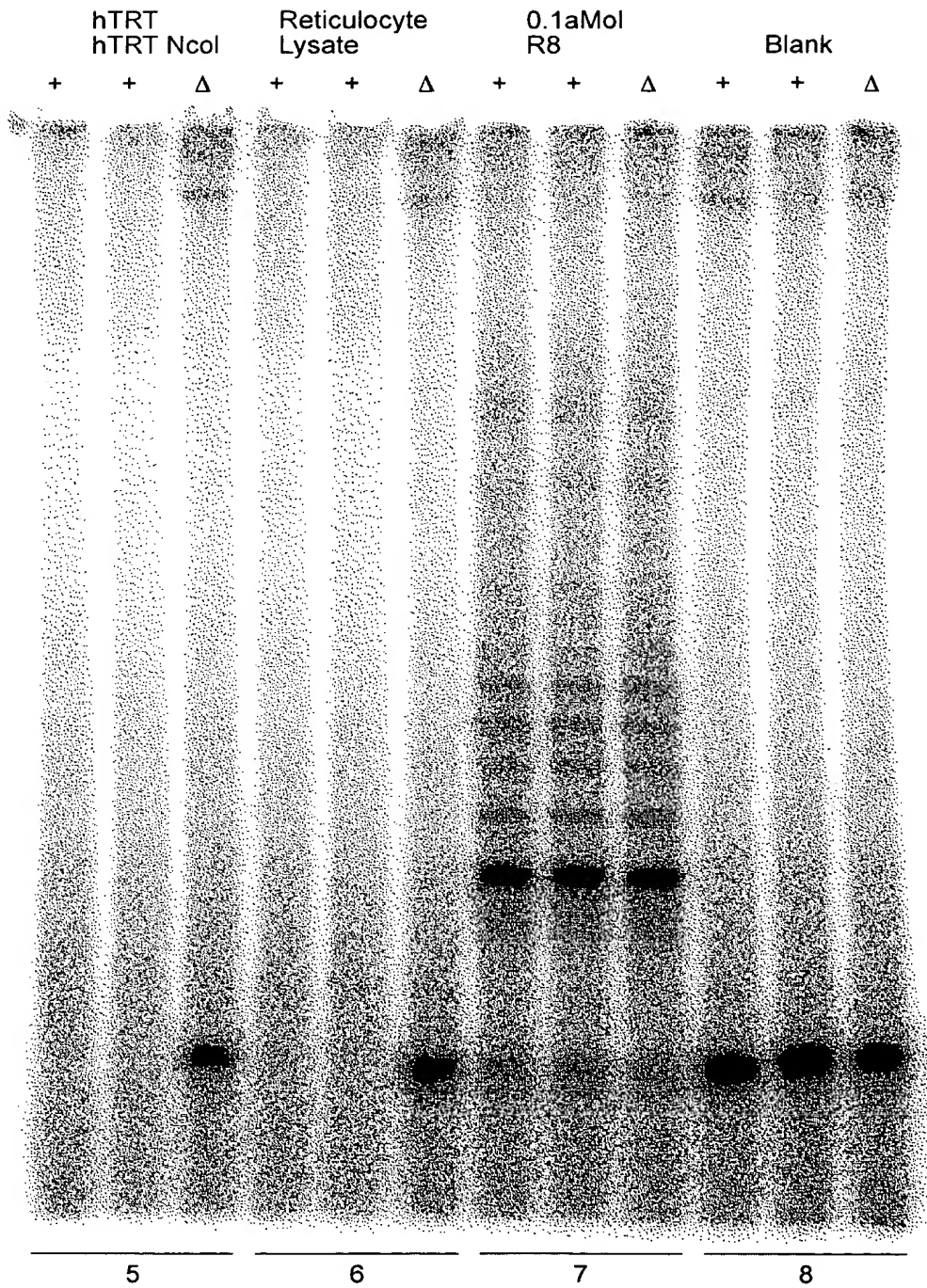


FIG. 10B

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11/103

Telomerase Specific Motifs

	MOTIF T	MOTIF T'
TRT con	W1	
hTRT	546 WLMSVYVVELLRSSFFVYVTE	Y Rk W 1 I E V
spTRT	429 WLNSFIIPILQSFYITESSDLNR	13 EAEVR
Ea_p123	441 WIFEDLVVSLIRCFYVTEQOKS	12 ENNVR
Sc_Est2	366 WLFRLIPKIIQTFYCTEISSTVT	12 EKEVE
		9 ENNVC

Telomerase RT Motifs (Fingers)

	MOTIF 1	MOTIF 2	MOTIF A	MOTIF B'
TRT con	R iPKk	fr I	p lyF D cYD i	Y q GIPQGs lS l Y
hTRT	11 SRLRFIPKPDG 0 LRPIV	69 PELYFVKVDVTGAYDTI	104 YVQCQGIPOGSSILSTLLCSLCY	
spTRT	10 AVIRLLPKKNT 0 FRLIT	66 RKKYFVRIDIKSCYDRI	99 YLQVGIPOGSSILSSFLCHFYM	
Ea_p123	10 GKRLIPKKT 0 FRPIM	67 PKLFFATMDIEKCYDSV	117 YKQTKGIPQGLCVSSILSSFY	
Sc_Est2	13 SKMRIIPKKS 2 FRIIA	68 PELYFMKFDVKSCYDSI	85 YIREDGLFQGSLSAPIVDLVY	
RT con	p hh h K	hR h	h hDh AF h	hPQG pP hh h
				GY

Telomerase RT Motifs (Palm, Primer Grip)

	MOTIF C	MOTIF D	MOTIF E
TRT con	lllrl Ddfl it	g	n K w g s l
hTRT	15 LLLRLVDDFLVLT	15 GVPEYGCVVNLRKTVV	24 WCGLLLDTRTL 192
spTRT	16 VLLRVVDDFLFIT	15 GFEKHNFTSLEKTVI	22 FFGFSVNMRS 176
Ea_p123	24 LLMRLTDDYLLIT	15 VSRENGFKFNKKLQT	28 WIGISIDMKTL 174
Sc_Est2	18 LILKLADDFLIIS	15 GFQKYNANRDKILA	25 WKHSSTMNHF 141
RT con	h Y DDhh	Gh h cK h	hLG h
	F		

FIG. 11

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12/103



181 GGACCCGGCGGCTTTCCGCGCGCTGGTGGCCAGTGCCTGGTGTGCGTGCCCTGGGACGC
CCTGGGCCGCCGAAAGGCGCGCGACCACGGGTACGGACCACACGCACGGGACCCTGCG

NFkB_CS1
GGGRQTYYYQC
NFkB-MHC-I.2
TGGGCTTCCCC

241 ACGGCCGCCCCCGCCGCCCCCTCCTTCCGCCAGGTGGGCCTCCCCGGGGTCGGCGTCCG
TGCCGGCGGGGGGCGCGGGGGAGGAAGGCGGTCCACCCGGAGGGGCCCCAGCCGCAGGC

Intron1

301 GCTGGGGTTGAGGGCGGCCGGGGGAACCAGCGACATGCGGAGAGCAGCGCAGGCGACTC
CGACCCCAACTCCCGCCGCCCCCCTTGGTCGCTGTACGCCTCTCGTCGCGTCCGCTGAG

NFkB_CS1
GGGRQTYYYQC
NFkB_CS2
RGGGRMTYYCC
Topo_II_cleavage_site
RN̄YNN̄C̄NNGYNGKTN̄NY

*****>

361 AGGGCGCTTCCCCCGCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGG
TCCCGCGAAGGGGGCGTCCACAGGACGGACTTCCTCGACCACGGGCTCACGACGTCTCC

FIG. 12

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1	AAAACCCCAA	AACCCCAAAA	CCCCTTTT	AGCCCTGCAG	TTGGAAATAT
51	AACCTCAGTA	TTAATAAGCT	CAGATTTTAA	ATATTAATTA	CAAAACCTAA
101	ATGGAGGTTG	ATGTTGATAA	TCAAGCTGAT	AATCATGGCA	TTCACTCAGC
151	TCTTAAGACT	TGTGAAGAAA	TTAAAGAAGC	TAAAACGTTG	TACTCTTGGA
201	TCCAGAAAGT	TATTAGATGA	AGAAATCAAT	CTCAAAGTCA	TTATAAAGAT
251	TTAGAAGATA	TTAAAAATATT	TGCGCAGACA	AATATTGTTG	CTACTCCACG
301	AGACTATAAT	GAAGAAGATT	TTAAAGTTAT	TGCAAGAAAA	GAAGTATTTT
351	CAACTGGACT	AATGATCGAA	CTTATTGACA	AATGCTTAGT	TGAACTTCTT
401	TCATCAAGCG	ATGTTTCAGA	TAGACAAAAA	CTTCAATGAT	TTGGATTTC
451	ACTTAAGGGA	AATCAATTAG	CAAAGACCCA	TTTATTAACA	GCTCTTTCAA
501	CTCAAAAGCA	GTATTTCTTT	CAAGACGAAT	GGAACCAAGT	TAGAGCAATG
551	ATTGGAAATG	AGCTCTTCCG	ACATCTCTAC	ACTAAATATT	TAATATTCCA
601	GCGAACTTCT	GAAGGAACTC	TTGTTCAATT	TTGCGGGAAT	AACGTTTTTG
651	ATCATTTGAA	AGTCAACGAT	AAGTTTGACA	AAAAGCAAAA	AGGTGGAGCA
701	GCAGACATGA	ATGAACCTCG	ATGTTGATCA	ACCTGCAAAAT	ACAATGTCAA
751	GAATGAGAAA	GATCACTTTC	TCAACAACAT	CAACGTGCCG	AATTGGAATA
801	ATATGAAATC	AAGAACCAGA	ATATTTTATT	GCACTCATTT	TAATAGAAAT
851	AACCAATTCT	TCAAAAAGCA	TGAGTTTGTG	AGTAACAAAA	ACAATATTTT
901	AGCGATGGAC	AGAGCTCAGA	CGATATTCAC	GAATATATTC	AGATTTAATA
951	GAATTAGAAA	GAAGCTAAAA	GATAAGGTTA	TCGAAAAAAT	TGCCTACATG
1001	CTTGAGAAAAG	TCAAAGATTT	TAACCTCAAC	TACTATTTAA	CAAATCTTG
1051	TCCTCTTCCA	GAAAATTTGGC	GGGAACGGAA	ACAAAAAATC	GAAAACCTGA
1101	TAAATAAAAC	TAGAGAAGAA	AAGTCGAAGT	ACTATGAAGA	GCTGTTTAGC
1151	TACACAACCTG	ATAATAAATG	CGTCACACAA	TTTATTAAATG	AATTTTTCTA
1201	CAATATACTC	CCCAAAGACT	TTTTGACTGG	AAGAAACCGT	AAGAATTTTC
1251	AAAAGAAAGT	TAAGAAATAT	GTGGAACATA	ACAAGCATGA	ACTCATTAC
1301	AAAAACTTAT	TGCTTGAGAA	GATCAATACA	AGAGAAATAT	CATGGATGCA
1351	GGTTGAGACC	TCTGCAAAGC	ATTTTTATTA	TTTTGATCAC	GAAAACATCT
1401	ACGTCTTATG	GAAATTGCTC	CGATGGATAT	TCGAGGATCT	CGTCGTCTCG
1451	CTGATTAGAT	GATTTTTCTA	TGTCACCGAG	CAACAGAAAA	GTTACTCCAA
1501	AACCTATTAC	TACAGAAAGA	ATATTTGGGA	CGTCATTATG	AAAATGTCAA
1551	TCGCAGACTT	AAAGAAGGAA	ACGCTTGCTG	AGGTCCAAGA	AAAAGAGGTT
1601	GAAGAATGGA	AAAAGTCGCT	TGGATTTGCA	CCTGGAAAAAC	TCAGACTAAT
1651	ACCGAAGAAA	ACTACTTTCC	GTCCAATTAT	GACTTTCAAT	AAGAAGATTG
1701	TAAATTTCAGA	CCGGAAGACT	ACAAAATTAA	CTACAAATAC	GAAGTTATTG
1751	AACTCTCACT	TAATGCTTAA	GACATTGAAG	AATAGAATGT	TTAAAGATCC
1801	TTTTGGATTG	GCTGTTTTTA	ACTATGATGA	TGTAATGAAA	AAGTATGAGG
1851	AGTTTGTTTG	CAAATGGAAG	CAAGTTGGAC	AACCAAAACT	CTTCTTTGCA
1901	ACTATGGATA	TCGAAAAGTG	ATATGATAGT	GTAAACAGAG	AAAACTATC
1951	AACATTCCTA	AAAACATACT	AATTACTTTC	TTCAAGATTTC	TGGATTATGA
2001	CTGCACAAAT	TCTAAAGAGA	AAGAATAACA	TAGTTATCGA	TTCGAAAAAC
2051	TTTAGAAAGA	AAGAAATGAA	AGATTATTTT	AGACAGAAAT	TCCAGAAGAT
2101	TGCACTTGAA	GGAGGACAAT	ATCCAACCTT	ATTCAAGTGT	CTTGAAAATG
2151	AACAAAATGA	CTTAAATGCA	AAGAAAACAT	TAATTGTTGA	AGCAAAGCAA
2201	AGAAATTTAT	TTAAGAAAGA	TAACCTACTT	CAACCAGTCA	TTAATATTTG
2251	CCAATTAAT	TACATTAAT	TTAATGGGAA	GTTTTATAAA	CAACAAAAAG
2301	GAATTCCTCA	AGGTCTTTGA	TTTTCATCAA	TTTTGTCATC	ATTTTATTAT
2351	GCAACATTAG	AGGAAAGCTC	CTTAGGATTC	CTTAGAGATG	AATCAATGAA

FIG. 13A



14/103

2401	CCCTGAAAAT	CCAAATGTTA	ATCTTCTAAT	GAGACTTACA	GATGACTATC
2451	TTTTGATTAC	AACTCAAGAG	AATAATGCAG	TATTGTTTAT	TGAGAAACTT
2501	ATAAACGTAA	GTCGTGAAAA	TGGATTTAAA	TTCAATATGA	AGAAACTACA
2551	GACTAGTTTT	CCATTAAGTC	CAAGCAAATT	TGCAAAATAC	GGAATGGATA
2601	GTGTTGAGGA	GCAAAATATT	GTTCAAGATT	ACTGCGATTG	GATTGGCATC
2651	TCAATTGATA	TGAAAACCTCT	TGCTTTAATG	CCAAATATTA	ACTTGAGAAT
2701	AGAAGGAATT	CTGTGTACAC	TCAATCTAAA	CATGCAAACA	AAGAAAGCAT
2751	CAATGTGGCT	CAAGAAGAAA	CTAAAGTCGT	TTTTAATGAA	TAACATTACC
2801	CATTATTTTA	GAAAGACGAT	TACAACCGAA	GACTTTGCGA	ATAAACTCT
2851	CAACAAGTTA	TTTATATCAG	GCGGTTACAA	ATACATGCAA	TGAGCCAAAG
2901	AATACAAGGA	CCACTTTAAG	AAGAACTTAG	CTATGAGCAG	TATGATCGAC
2951	TTAGAGGTAT	CTAAAATTAT	ATACTCTGTA	ACCAGAGCAT	TCTTTAAATA
3001	CCTTGTGTGC	AATATTAAGG	ATACAATTTT	TGGAGAGGAG	CATTATCCAG
3051	ACTTTTTCCT	TAGCACACTG	AAGCACTTTA	TTGAAATATT	CAGCACAAAA
3101	AAGTACATTT	TCAACAGAGT	TTGCATGATC	CTCAAGGCAA	AAGAAGCAAA
3151	GCTAAAAAGT	GACCAATGTC	AATCTCTAAT	TCAATATGAT	GCATAGTCGA
3201	CTATTCTAAC	TTATTTTGGG	AAGTTAATTT	TCAATTTTGT	TCTTATATAC
3251	TGGGGTTTTG	GGGTTTTGGG	GTTTTGGGG		

FIG. 13B

1	MEVDVDNQAD	NHGIHSALKT	CEEIKEAKTL	YSWQKQVIRC	RNQSQSHYKD
51	LEDIKIFAQT	NIVATPRDYN	EEDFKVIARK	EVFSTGLMIE	LIDKCLVELL
101	SSSDVSDRQK	LQCFGFQLKG	NQLAKTHLLT	ALSTQKQYFF	QDEWNQVRAM
151	IGNELFRHLY	TKYLIFORTS	EGTLVQFCGN	NVFDHLKVND	KFDKKQKGGG
201	ADMNEPRCCS	TCKYNVKNEK	DHFLNNINVP	NWNNMKSRT	IFYCTHFNRN
251	NQFFKKHEFV	SNKNNISAMD	RAQTIFTNIF	RFNRIRKKLK	DKVIEKIAM
301	LEKVKDFNFN	YYLTKSCPLP	ENWRERKQKI	ENLINKTREE	KSKYEEELFS
351	YTTDNKCVTQ	FINEFFYNIL	PKDFLTGRNR	KNFQKKVKKY	VELNKHელი
401	KNLLLEKINT	REISWMQVET	SAKHFFYFDH	ENIYVLWKLL	RWIFEDLVVS
451	LIRCFYVTE	QQKSYSKTY	YRKNWDVIM	KMSIADLKKE	TLAEVQEKEV
501	EEWKSLGFA	PGKLRLIPKK	TTFRPIMTFN	KKIVNSDRKT	TKLTTNTKLL
551	NSHMLKTLK	NRMFKDPFGF	AVFNYDDVMK	KYEEFVCKWK	QVGQPKLFFA
601	TMDIEKCYDS	VNREKLSTFL	KTTKLLSSDF	WIMTAQILKR	KNNIVIDSKN
651	FRKKEMKDYF	RQKFQKIALE	GGQYPTLFSV	LENEQNDLNA	KKTLIVEAKQ
701	RNYFKDNL	QPVINICQYN	YINFNGKFYK	QTKGIPQGLC	VSSILSSFY
751	ATLEESSLGF	LRDESMNPEN	PNVNLLMRLT	DDYLLITTQE	NNAVLFIEKL
801	INVSRENGFK	FNMKKLQTSF	PLSPSKFAKY	GMDSVEEQNI	VQDYCDWIGI
851	SIDMKTLALM	PNINLRIEGI	LCTLNLMQ	KKASMWLKKK	LKSFLMNNIT
901	HYFRKTIITE	DFANKTLNKL	FISGGYKYM	CAKEYKDHFK	KNLAMSSMID
951	LEVSKIIVSV	TRAFKYLVC	NIKDTIFGEE	HYPDFFLSTL	KHFIEIFSTK
1001	KYIFNRVCM	LKAKEAKLKS	DQCQSLIQYD	A	

FIG. 14



16/103

1470 GAT CTC GTT TCT ACT TTT CCT AAT TAC CTT ATA TCT ATA CTT GAG TCA AAA AAT TGG CAA 1529
129 D L V S T F P N Y L I S I L E S K N W Q 148
1530 CTT TTG TTA GAA AT gtaataaccgggttaagatgttgcgactttgaacaagactgacaagtatag T ATC GGC 1601
149 L L L E I I G 155
1602 AGT GAT GCC ATG CAT TAC TTA TTA TCC AAA GGA AGT ATT TTT GAG GCT CTT CCA AAT GAC 1661
156 S D A M H Y L L S K G S I F E A L P N D 175
1662 AAT TAC CTT CAG ATT TCT GGC ATA CCA CTT TTT AAA AAT AAT GTG TTT GAG GAA ACT GTG 1721
176 N Y L Q I S G I P L F K N N V F E T V 195
1722 TCA AAA AGA AAG CGA ACC ATT GAA ACA TCC ATT ACT CAA AAT AAA AGC GCC CGC AAA 1781
196 S K K R K R T I E T S I T Q N K S A R K 215
1782 GAA GTT TCC TGG AAT AGC ATT TCA ATT AGT AGG TTT AGC ATT TTT TAC AGG TCA TCC TAT 1841
216 E V S W N S I S I S R F S I F Y R S S Y 235
1842 AAG AAG TTT AAG CAA G gtaactaactgttatccttcataactaatttttag AT CTA TAT TTT AAC 1907
236 K K F K Q D L Y F N 245
1908 TTA CAC TCT ATT TGT GAT CGG AAC ACA GTA CAC ATG TGG CTT CAA TGG ATT TTT CCA AGG 1967
246 L H S I C D R N T V H M W L Q W I F P R 265
1968 CAA TTT GGA CTT ATA AAC GCA TTT CAA GTG AAG CAA TTG CAC AAA GTG ATT CCA CTG GTA 2027
266 Q F G L I N A F Q V K Q L H K V I P L V 285
2028 TCA CAG AGT ACA GTT GTG CCC AAA CGT CTC CTA AAG GTA TAC CCT TTA ATT GAA CAA ACA 2087
286 S Q S T V V P K R L L K V Y P L I E Q T 305
2088 GCA AAG CGA CTC CAT CGT ATT TCT CTA TCA AAA GTT TAC AAC CAT TAT TGC CCA TAT ATT 2147
306 A K R L H R I S L S K V Y N H Y C P Y I 325
2148 GAC ACC CAC GAT GAT GAA AAA ATC CTT AGT TAT TCC TTA AAG CCG AAC CAG GTG TTT GCG 2207
326 D T H D D E K I L S Y S L K P N Q V F A 345
2208 TTT CTT CGA TCC ATT CTT GTT CGA GTG TTT CCT AAA TTA ATC TGG GGT AAC CAA AGG ATA 2267
346 F L R S I L V R V F P K L I W G N Q R I 365

FIG. 15B



17/103

2268 TTT GAG ATA ATA TTA AAA G gatttgataaaattttattaccactaacgattttaccag AC CTC GAA ACT 2336
366 F E I I L K D L E T 375
2337 TTC TTG AAA TTA TCG AGA TAC GAG TCT TTT AGT TTA CAT TAT TTA ATG AGT AAC ATA AAG 2396
376 F L K L S R Y E S F S L H Y L M S N I K 395
2397 gtaatatgcaaaattttttaccattaattaacaatcag ATT TCA GAA ATT GAA TGG CTA GTC CTT GGA 2465
396 I S E I E W L V L G 405
2466 AAA AGG TCA AAT GCG AAA ATG TGC TTA AGT GAT TTT GAG AAA CGC AAG CAA ATA TTT GCG 2525
406 K R S N A K M C L S D F E K R K Q I F A 425
2526 GAA TTC ATC TAC TGG CTA TAC AAT TCG TTT ATA ATA CCT ATT TTA CAA TCT TTT TTT TAT 2585
426 E F I Y W L Y N S F I I P I L Q S F F Y 445
2586 ATC ACT GAA TCA AGT GAT TTA CGA AAT CGA ACT GTT TAT TTT AGA AAA GAT ATT TGG AAA 2645
446 I T E S S D L R N R T V Y F R K D I W K 465
2646 CTC TTG TGC CGA CCC TTT ATT ACA TCA ATG AAA ATG GAA GCG TTT GAA AAA ATA AAC GAG 2705
466 L L C R P F I T S M K M E A F E K I N E 485
2706 gtattttaaggtatttttttgcaaaaagctaatttttcag AAC AAT GTT AGG ATG GAT ACT CAG AAA ACT 2775
486 N N V R M D T Q K T 495
2776 ACT TTG CCT CCA GCA GTT ATT CGT CTA TTA CCT AAG AAG AAT ACC TTT CGT CTC ATT ACG 2835
496 T L P P A V I R L L P K K N T F R L I T 515
2836 AAT TTA AGA AAA AGA TTC TTA ATA AAG gtatttaatttttggtcatcaatgtacttttacttctaattatta 2906
516 N L R K R F L I K 524
2907 ttagcag ATG GGT TCA AAC AAA AAA ATG TTA GTC AGT ACG AAC CAA ACT TTA CGA CCT GTG 2967
525 M G S N K K M L V S T N Q T L R P V 542
2968 GCA TCG ATA CTG AAA CAT TTA ATC AAT GAA AGT AGT GGT ATT CCA TTT AAC TTG GAG 3027
543 A S I L K H L I N E S S G I P F N L E 562
3028 GTT TAC ATG AAG CTT ACT TTT AAG AAG GAT CTT CTT AAG CAC CGA ATG TTT GG gtaat 3088
563 V Y M K L L T F K K D L L K H R M F G 581

FIG. 15C



18/103

3089 tatataatgcgatccctcattattattgag G CGT AAG AAG TAT TTT GTA CGG ATA GAT ATA 3155
582 R K K Y F V R I D I 591

3156 AAA TCC TGT TAT GAT CGA ATA AAG CAA GAT TTG ATG TTT CGG ATT GTT AAA AAG AAA CTC 3215
592 K S C Y D R I K Q D L M F R I V K K L 611

3216 AAG GAT CCC GAA TTT GTA ATT CGA AAG TAT GCA ACC ATA CAT GCA ACA AGT GAC CGA GCT 3275
612 K D P E F V I R K Y A T I H A T S D R A 631

3276 ACA AAA AAC TTT GTT AGT GAG GCG TTT TCC TAT T gtaagtttttttttttcattggaattttttaacaa 3343
632 T K N F V S E A F S Y F 643

3344 attcttttttag TT GAT ATG GTG CCT TTT GAA AAA GTC GTG CAG TTA CTT TCT ATG AAA ACA 3405
644 D M V P F E K V V Q L L S M K T 659

3406 TCA GAT ACT TTG TTT GTT GAT TTT GTG GAT TAT TGG ACC AAA AGT TCT TCT GAA ATT TTT 3465
660 S D T L F V D F V D Y W T K S S S E I F 679

3466 AAA ATG CTC AAG GAA CAT CTC TCT GGA CAC ATT GTT AAG gtataccaattgtgaattgtaataaca 3532
680 K M L K E H L S G H I V K 692

3533 ctaatgaaactag ATA GGA AAT TCT CAA TAC CTT CAA AAA GTT GGT ATC CCT CAG GGC TCA 3593
693 I G N S Q Y L Q K V G I P Q G S 708

3594 ATT CTG TCA TCT TTT TTG TGT CAT TTC TAT ATG GAA GAT TTG ATT GAT GAA TAC CTA TCG 3653
709 I L S S F L C H F Y M E D L I D E Y L S 728

3654 TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA GTA GTC GAC GAT TTC CTC TTT ATA ACA 3713
729 F T K K G S V L L R V V D D F L F I T 748

3714 GTT AAT AAA AAG GAT GCA AAA AAA TTT TTG AAT TTA TCT TTA AGA G gtgagttgtgtcattcc 3777
749 V N K K D A K K F L N L S L R G 764

3778 taagttctaacggttgaag GA TTT GAG AAA CAC AAT TTT TCT ACG AGC CTG GAG AAA ACA GTA 3840
765 F E K H N F S T S L E K T V 778

3841 ATA AAC TTT GAA AAT AGT AAT GGG ATA ATA AAC AAT ACT TTT TTT AAT GAA AGC AAG AAA 3900
779 I N F E N S N G I I N N T F F N E S K K 798

FIG. 15D



19/103

3901 AGA ATG CCA TTC TTC GGT TTC TCT GTG AAC ATG AGG TCT CTT GAT ACA TTG TTA GCA TGT 3960
799 R M P F F G F S V N M R S L D T L L A C 818
3961 CCT AAA ATT GAT GAA GCC TTA TTT AAC TCT ACA TCT GTA GAG CTG ACG AAA CAT ATG GGG 4020
819 P K I D E A L F N S T S V E L T K H M G 838
4021 AAA TCT TTT TTT TAC AAA ATT CTA AG gtatactgtgtaactgaataatagctgacaaataatcag A TCG 4089
839 K S F F Y K I L R S 848
4090 AGC CTT GCA TCC TTT GCA CAA GTA TTT ATT GAC ATT ACC CAC AAT TCA AAA TTC AAT TCT 4149
849 S L A S F A Q V F I D I T H N S K F N S 868
4150 TGC TGC AAT ATA TAT AGG CTA GGA TAC TCT ATG TGT ATG AGA GCA CAA GCA TAC TTA AAA 4209
869 C C N I Y R L G Y S M C M R A Q A Y L K 888
4210 AGG ATG AAG GAT ATA TTT ATT CCC CAA AGA ATG TTC ATA ACG G gtgagtactttttaactaga 4274
889 R M K D I F I P Q R M F I T D 903
4275 aaagtcattaattaaccccttag AT CTT TTG AAT GTT ATT GGA AGA AAA ATT TGG AAA AAG TTG GCC 4339
904 L L N V I G R K I W K K L A 917
4340 GAA ATA TTA GGA TAT ACG AGT AGG CGT TTC TTG TCC TCT GCA GAA GTC AAA TG gtacgtgtc 4401
918 E I L G Y T S R R F L S S A E V K W 935
4402 ggctcgcgagacttcagcaaatattgacacacatcag G CTT TTT TGT CTT GGA ATG AGA GAT GGT TTG AAA 4468
936 L F C L G M R D G L K 946
4469 CCC TCT TTC AAA TAT CAT CCA TGC TTC GAA CAG CTA ATA TAC CAA TTT CAG TCA TTG ACT 4528
947 P S F K Y H P C F E Q L I Y Q F Q S L T 966
4529 GAT CTT ATC AAG CCG CTA AGA CCA GTT TTG CGA CAG GTG TTA TTT TTA CAT AGA ATA 4588
967 D L I K P L R P V L R Q V L F L H R R I 986
4589 GCT GAT TAA tgtcatttttcaattattattatatatacatcccttttactgtgtgtctttaaacaaatattattactaagtata 4665
987 A D * 989

FIG. 15E

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4666 gctgacccccaaagcaagcatactataggatttcttagtaaaagtaaaaataatctcgttattagtttttgacttgtct 4745
4746 ttatccttatacttttaagaaaagattgacagtggttgctgactactgcccacatgcccattaaaacgggagtggttaaca 4825
4826 ttaaaagtaatacatgaggctaatactcctttcatTTagaataaggaagtggTTTTctataatgaataatgccgcacta 4905
4906 atgcaaaaagacgaagattatcttctaaacaaggggatTaagcatatccgaagaaaagagagtaataaccagtgtt 4985
4986 gttgaagaaagcaaggataatttggaacaagcttctgcagatgacaggctaaattttggtagccgaattttggtaaaaagc 5065
5066 cccaggttatccatggtggccggccttgctactgagacgaaaagaaactaaaggatagtttgaataactaatagctcattta 5145
5146 atgtcttatataaggttttggTTTTcctgacttcaatttgcatgggtgaaaagaaatagtgTTaagccattattggat 5225
5226 tccgaaatagccaaatttcttggttccctcaaacgggaagtctaaagaacttattgaagcttatgaggcttcaaaaactcc 5305
5306 tcctgatttaaggagggaatcttccacgatgaggaatggatagcttatcagctgctgaggagaaagcctaattttttgc 5385
5386 aaaaagaaaaataTcaltgggagacatctcttgatgaatcagatcggaagagtatctccagcggatccttgatgtcaata 5465
5466 acttctatttctgaaatgtatggTcctactgtcgcttcgacttctcgtagctctacgcagttaaagtgaccaaaggTacc 5544

FIG. 15F

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1	gcagegctgc	gtcctgctgc	gcacgtggga	agccctggcc	ccggccaccc	ccgcgatgcc
61	gcgcgctccc	cgctgcccag	ccgtgcccgc	cctgctgcgc	agccactacc	gcgaggtgct
121	gccgctggcc	acgttccgtgc	ggcgccctggg	gccccagggc	tgccggtggt	tgccagcgccg
181	ggaccocggcg	gctttccgcg	cgctgggtggc	ccagtgcctg	gtgtgcgtgc	cctgggacgc
241	acggccgccc	cccgccgccc	cctccttccg	ccaggtgtcc	tgccgaagg	agctggtggc
301	ccgagtgctg	cagaggtggt	gcgagcgccg	cgcaagaac	gtgctggcct	tcggcttcgc
361	gctgctggac	ggggcccgccg	ggggccccc	cgaggccttc	accaccagcg	tgccagcta
421	cctgccccaac	acggtagccg	acgcactgcg	ggggagcgccg	gcgtgggggc	tgctgctgcg
481	ccgcgtgggg	gacgacgtgc	tggttcacct	gctggcacgc	tgccgctct	ttgtgctggt
541	ggctcccagc	tgccgctacc	aggtgtgccc	gcccgcgctg	taccagctcg	gcgtgcccac
601	tcaggcccg	cccccgccac	acgctagtgg	accccgaagg	cgtctgggat	gcgaacgggc
661	ctggaaccat	agcgtcaggg	aggccggggg	ccccctgggc	ctgccagccc	cggtgcccag
721	gaggcgccgg	ggcagtgcca	gcccgaagtct	gcccgtggcc	aagaggccca	ggcgtggccg
781	tgccctgag	ccggagcgga	cgcccgctgg	gcagggggtcc	tgggccccc	cgggcaggac
841	gcgtggaccg	agtgaacgtg	gtttctgtgt	gggtgtcacct	gcccagaccg	cggaagaagc
901	cacctctttg	gaggggtgccc	tctctggcac	gcgccactcc	caccatccg	tgggccgcca
961	gcaccacgcg	ggccccccat	ccacatcgcc	gccaccacgt	ccctgggaca	cgcttctgtcc
1021	cccggtgtac	gcccagacca	agcacttccc	ctactcctca	ggcgacaagg	gcagccctgcg
1081	gcccctccttc	ctactcagct	ctctgagggc	cagcctgact	ggcgctcgga	ggctcgtgga
1141	gaccatcttt	ctgggttcca	ggccctggat	gccagggact	ccccgcaggt	tgccccgcct
1201	gccccagcgc	tactggcaaa	tgccggccct	gtttctggag	ctgcttggga	accacgcgca
1261	gtgccccctac	gggggtgctcc	tcaagacgca	ctgcccgcgtg	cgagctgcgg	tcaccccagc
1321	agccggtgtc	tgtgcccggg	agaagcccca	gggctctgtg	gcggccccc	aggaggaggga
1381	cacagacccc	cgctgcctgg	tgacgtgct	ccgccagcac	agcagccct	ggcaggtgta
1441	cggttccgtg	cgggcctgccc	tgccgcggct	gggtgccccca	ggcctctggg	gctccaggca
1501	caacgaacgc	cgcttccctca	ggaacaccaa	gaagtccatc	tccttgggga	agcatgccaa
1561	gctctcgtg	caggagctga	cggtgaagat	gagcgtgcgg	gactgcgctt	ggctgcgcag
1621	gagcccagg	gttggctgtg	ttccggccgc	agagcacctg	ctgcgtgagg	agatcctggc
1681	caagtccctg	cactggctga	tgagtggtga	cgctcgtcag	ctgctcaggt	cttctcttta
1741	tgctacggag	accacgtttc	aaaagaacag	gctctttttc	taccggaaga	gtgtctggag
1801	caagtgtcaa	agcattggaa	tcagacagca	cttgaagagg	gtgcagctgc	gggagctgtc
1861	ggaagcagag	gtcaggcagc	atcggaagc	caggcccgc	ctgctgacgt	ccagactccg
1921	cttccatccc	aagcctgacg	ggctgcggcc	gattgtgaac	atggactacg	tcgtgggagc
1981	cagaacgttc	cgcagagaaa	agagggccga	gcgtctcacc	tcgaggtgta	aggcactggt
2041	cagcgtgctc	aactacgagc	gggcgcggcg	ccccggcctc	ctggggcctg	ctgtgctggg
2101	cctggacgat	atccacaggg	cctggcgcac	cttctgtgctg	cgctgcccgt	cccaggaccc
2161	gcccgcctgag	ctgtactttg	tcaaggtgga	tgtgacgggc	gcgtacgaca	ccatccccc
2221	ggacaggctc	acggaggtca	tcgccagcat	catcaaacc	cagaacacgt	actgcgtgcg
2281	tcgggtatgcc	gtgggtccaga	aggccgccc	tgggcacgtc	cgcaaggcct	tcaagagcca
2341	cgtctctacc	ttgacagacc	tcagccgcta	catgcgacag	ttcgtggctc	acctgcagga
2401	gaccagcccg	ctgagggatg	ccgtcgtcat	cgagcagagc	tcctccctga	atgaggccag
2461	cagtggcctc	ttcagcgtct	tcctacgctt	catgtgccac	cacgccgtgc	gcacagggg
2521	caagtccctac	gtccagtgcc	aggggatccc	cgagggtccc	atcctctcca	cgctgctctg
2581	cagcctgtgc	tacggcgaca	tggaagaaca	gctgtttgcg	gggattccgc	gggacgggct
2641	gctcctgcgt	ttgggtggatg	atttcttgtt	gggtgacacct	cacctcaccc	acgcgaaaac
2701	cttccctcagg	accctggctc	gaggtgtccc	tgagtatggc	tgctgtggta	acttccggaa
2761	gacagtgggtg	aacttccctg	tagaagacga	ggccctgggt	ggcacggctt	ttgttcagat
2821	gcccggccac	ggcctattcc	cctggtgccc	cctgctgctg	gatacccgga	ccctggagggt
2881	gcagagcgac	tactccagct	atgcccggac	ctccatcaga	gccagtctca	ccttcaaccg
2941	cggttccaag	gctgggagga	acatgcgtcg	caaaactctt	ggggctcttg	ggctgaagtg
3001	tcacagcctg	tttctggatt	tgacaggtga	cagcctccag	acggtgtgca	ccaacatcta
3061	caagatcctc	ctgctgcagg	cgtacaggtt	tcacgcatgt	gtgctgcagc	tcccatttca
3121	tcagcaagtt	tggaagaacc	ccacattttt	cctgcgcgtc	atctctgaca	cggcctccct
3181	ctgctactcc	atcctgaaag	ccaagaacgc	agggatgtcg	ctgggggcca	aggcgccgc
3241	cgccctctg	ccctccgagg	ccgtgcagtg	gctgtgccac	caagcattcc	tgctcaagct
3301	gactgcacac	cgtgtcacct	acgtgccact	cctgggggtca	ctcaggacag	cccagacgca
3361	gctgagtcgg	aagctcccgg	ggacgacgct	gactgcccgtg	gagggccgag	ccacccggc
3421	actgccctca	gacttcaaga	ccatcctgga	ctgatggcca	cccgccaca	gccaggccga
3481	gagcagacac	cagcagccct	gtcacgccc	gctctacgtc	ccagggaggg	agggggcgcc
3541	cacacccagg	cccgcaccgc	tgggagtctg	aggcctgagt	gagtggttgg	cgaagccctg
3601	catgtccggc	tgaaggctga	gtgtccggct	gagggcctgag	cgagtgtcca	gccaagggct
3661	gagtgtccag	cacacctgcc	gtcttcaact	ccccacaggc	tgccgctcgg	ctccacccca
3721	gggccaagctt	ttcctcacca	ggagccggc	ttccactccc	cacataggaa	tagtccatcc
3781	ccagattcgc	cattgtttcac	ccctgcctcc	gcctcctttt	gcctccacc	ccacccatcc
3841	aggtggagac	cctgagaagg	accctgggag	ctctgggaat	ttggagtgc	caaaggtgtg
3901	ccctgtacac	aggcgaggac	cctgcacctg	gatgggggtc	cctgtgggtc	aaattggggg
3961	gaggtgctgt	gggagtaaaa	tactgaatat	atgagttttt	cagttttgaa	aaaaa

FIG. 16

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22/103

MPRAPRCRAVRSLLRSHYREVLPLATFVRRLLGPQGWRLVQRGDP
 AAFRALVAQCLVCVPWDARPPPAAPSFRQVSCLELVARVLQRL
 CERGAKNVLAFGFALLDGAAGGPPEAFTTSVRSYLPNTVTDALR
 GSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLY
 QLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPG
 ARRRGGSASRSLPLPKRPRRGAAPEPERTVPGQGSWAHPGRTRG
 PSDRGFCVVSPPARPAEEATSLEGALSGTRHSHPSVGRQHAGPP
 STSRPPRPWDTPCPPVYAETKHFYSSGDKEQLRPSFLLSSLRP
 SLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLEL
 LGNHAQCPYGVLLKTHCPLRAAVTPAAGVCAREKPQGSVAAPEE
 EDTDPRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGSRHNE
 RRFLRNTKKFISLGKHAKLSELQELTWKMSVRDCAWLRSPGVGC
 VPAAEHLRLREEILAKFLHWMMSVYVVELLRSFFYYVTEFTFQKNR
 LFFYRKSVWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPAL
 LTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA
 LFSVLNYERARRPGLLGASVGLDDIHRARWTFVLRVRAQDPPP
 ELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQ
 KAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVI
 EQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGI PQGSI
 LSTLLCSLCYGD MENKLFAGIRRDGLLLRLVDDFLLVTPHLTHA
 KTFRLTLVRGVPEYGCVVNLKRTVVNFPVEDEALGGTAFVQMPA
 HGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTFNRGFKAGR
 NMRRKLFGLVRLKCHSLFLDLQVNSLQTVCTNIYKILLQLQAYRF
 HACVLQLPFHQVWKNPTFFLRVISDTASLCYSILKAKNAGMSL
 GAKGAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLGLSLRTAQ
 TQLSRKLPGTTLTALEAAANPALPSDFKTILD

FIG. 17

GGCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTT
 TTATGTACAGGAGACCACGTTTCAAAGAAGCAGGCTCTTTTTCTACCGGAAGAGTGTCTG
 GAGCAAGTTGCAAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGACGTGCGGGAGCT
 GTCGGAAGCAGAGGTGAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACT
 CCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCTGTTGG
 AGCCAGAAGCTTCCGAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACT
 GTTCAGCGTGCTCAACTACGAGCGGGCGCGGCCCGCCCTCTGTTGGCGCCCTCTGTGCT
 GGGCCTGGACGATATCCACAGGGCTGCGGCACCTTCGTGCTGCGTGTGCGGGCCAGGA
 CCGCGCCGCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCC
 CCAGGACAGGCTCACGGAGGTTCATCGCCAGCATCATCAAACCCAGAACACGTACTGCGT
 GCGTGGTATGCGGTGGTCCAGAAGGCCGCCATGGGCACGTCCGCAAGGCCCTCAAGAG
 CCACGTCTCAGTCCAGTGCCAGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCT
 GCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGGCGGGGATTGCGCGGGACGGC
 TGCTCCTGCGTTTGGTGGATGATTTCTTGTGGTGACACCTCACCTCACCCACGCGAAAA
 CCTTCTCAGGACCTTGGTCCGAGGTGTCCCTGAGTATGGTGGTGGTGAACCTTGGCGGA
 AGACAGCTGGTGAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTGTTCAGA
 TGCCGGCCACGGCCTATTTCCCTGGTGGCGCTGCTGCTGGATACCCGGACCTGGAGG
 TGCAGAGCGACTACTCCAGCTATGCCCCGACCTCCATCAGAGCCAGTCTCACCTCAACC
 GCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACCTTTTGGGGTCTTGGCGCTGAAGT
 GTCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCT
 ACAAGATCCTCCTGCTGCAGGCGTACAGGTTTACGCATGTGTGCTGCAGCTCCCATTTT
 ATCAGCAAGTTTGAAGAACCCACATTTTCTGCGCGTCATCTCTGACACGGCCTCCC
 TCTGCTACTCCATCTGAAAGCCAAGAAGCAGGGATGTCGCTGGGGGCCAAGGGCGCCG
 CCGGCC7TCTGCCCTCCGAGGCCGTGAGTGGCTGTGCCACCAAGCATTCTGCTCAAGC
 TGACTCGACACCGTGTACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCAGACGC
 AGCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGAGCCAAACCCG
 CACTGCCCTCAGACTTCAAGACCATCTGGACTGATGGCCACCCGCCACAGCCAGGCCG
 AGACAGACACCCAGCAGCCCTGTACGCCGGGCTCTACGTCCAGGGAGGGAGGGGGCGG
 CCACACCCAGGCTGCACCGCTGGGAGTCTGAGGCTGAGTGAGTGTGGCGGAGGCTT
 GCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGC
 TGAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCC
 AGGGCAGCTTTTCTCACCAGGAGCCCGCTTCACTCCCCACATAGGAATAGTCCATC
 CCCAGATTGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT
 CAGGTGGAGACCTGAGAAGGACCTGGGAGCTCTGGGAATTTGGAGTGACCAAGGTGT
 GCCCTGTACACAGGCGAGGACCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTTGGGG
 GGAGGTGCTGTGGGAGTAAATACTGAATATATGAGTTTTTCACTTTTGTGAAAAA
 AAAAAAAAAAAAAA

FIG. 18

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23/103



MetSerValTyrValValGluLeuLeuArgSerPhePhe
 TyrValThrGluThrThrPheGlnLysAsnArgLeuPhe
 PheTyrArgLysSerValTrpSerLysLeuGlnSerIle
 GlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu
 LeuSerGluAlaGluValArgGlnHisArgGluAlaArg
 ProAlaLeuLeuThrSerArgLeuArgPheIleProLys
 ProAspGlyLeuArgProIleValAsnMetAspTyrVal
 ValGlyAlaArgThrPheArgArgGluLysArgAlaGlu
 ArgLeuThrSerArgValLysAlaLeuPheSerValLeu
 AsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAla
 SerValLeuGlyLeuAspAspIleHisArgAlaTrpArg
 ThrPheValLeuArgValArgAlaGlnAspProProPro
 GluLeuTyrPheValLysValAspValThrGlyAlaTyr
 AspThrIleProGlnAspArgLeuThrGluValIleAla
 SerIleIleLysProGlnAsnThrTyrCysValArgArg
 TyrAlaValValGlnLysAlaAlaHisGlyHisValArg
 LysAlaPheLysSerHisValLeuArgProValProGly
 AspProAlaGlyLeuHisProLeuHisAlaAlaLeuGln
 ProValLeuArgArgHisGlyGluGlnAlaValCysGly
 AspSerAlaGlyArgAlaAlaProAlaPheGlyGly

FIG. 19

1
met

GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCG ATG

10

pro arg ala pro arg cys arg ala val arg ser leu leu arg ser
 CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC

20

his tyr arg glu val leu pro leu ala thr phe val arg arg leu
 CAC TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG

30

40

gly pro gln gly trp arg leu val gln arg gly asp pro ala ala
 GGG CCC CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT

50

60

phe arg ala leu val ala gln cys leu val cys val pro trp asp
 TTC CGC GCG CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC

70

ala arg pro pro pro ala ala pro ser phe arg gln val ser cys
 GCA CGG CCG CCC CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC

80

90

leu lys glu leu val ala arg val leu gln arg leu cys glu arg
 CTG AAG GAG CTG GTG GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC

100

gly ala lys asn val leu ala phe gly phe ala leu leu asp gly
 GGC GCG AAG AAC GTG CTG GCC TTC GGC TTC GCG CTG CTG GAC GGG

110

120

ala arg gly gly pro pro glu ala phe thr thr ser val arg ser
 GCC CGC GGG GGC CCC CCC GAG GCC TTC ACC ACC AGC GTG CGC AGC

FIG. 20A

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24/103



130
 tyr leu pro asn thr val thr asp ala leu arg gly ser gly ala
 TAC CTG CCC AAC ACG GTG ACC GAC GCA CTG CGG GGG AGC GGG GCG

140
 trp gly leu leu leu arg arg val gly asp asp val leu val his
 TGG GGG CTG CTG CTG CGC CGC GTG GGC GAC GAC GTG CTG GTT CAC

150
 leu leu ala arg cys ala leu phe val leu val ala pro ser cys
 CTG CTG GCA CGC TGC GCG CTC TTT GTG CTG GTG GCT CCC AGC TGC

160
 ala tyr gln val cys gly pro pro leu tyr gln leu gly ala ala
 GCC TAC CAG GTG TGC GGG CCG CCG CTG TAC CAG CTC GGC GCT GCC

170
 thr gln ala arg pro pro pro his ala ser gly pro arg arg arg
 ACT CAG GCC CGG CCC CCG CCA CAC GCT AGT GGA CCC CGA AGG CGT

180
 leu gly cys glu arg ala trp asn his ser val arg glu ala gly
 CTG GGA TGC GAA CGG GCC TGG AAC CAT AGC GTC AGG GAG GCC GGG

190
 val pro leu gly leu pro ala pro gly ala arg arg arg gly gly
 GTC CCC CTG GGC CTG CCA GCC CCG GGT GCG AGG AGG CGC GGG GGC

200
 ser ala ser arg ser leu pro leu pro lys arg pro arg arg gly
 AGT GCC AGC CGA AGT CTG CCG TTG CCC AAG AGG CCC AGG CGT GGC

210
 ala ala pro glu pro glu arg thr pro val gly gln gly ser trp
 GCT GCC CCT GAG CCG GAG CGG ACG CCC GTT GGG CAG GGG TCC TGG

220
 ala his pro gly arg thr arg gly pro ser asp arg gly phe cys
 GCC CAC CCG GGC AGG ACG CGT GGA CCG AGT GAC CGT GGT TTC TGT

230
 val val ser pro ala arg pro ala glu glu ala thr ser leu glu
 GTG GTG TCA CCT GCC AGA CCC GCC GAA GAA GCC ACC TCT TTG GAG

240
 gly ala leu ser gly thr arg his ser his pro ser val gly arg
 GGT GCG CTC TCT GGC ACG CGC CAC TCC CAC CCA TCC GTG GGC CGC

250
 gln his his ala gly pro pro ser thr ser arg pro pro arg pro
 CAG CAC CAC GCG GGC CCC CCA TCC ACA TCG CGG CCA CCA CGT CCC

260
 trp asp thr pro cys pro pro val tyr ala glu thr lys his phe
 TGG GAC ACG CCT TGT CCC CCG GTG TAC GCC GAG ACC AAG CAC TTC

270
 320
 330

FIG. 20B

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25/103

340
leu tyr ser ser gly asp lys glu gln leu arg pro ser phe leu
CTC TAC TCC TCA GGC GAC AAG GAG CAG CTG CGG CCC TCC TTC CTA

350
leu ser ser leu arg pro ser leu thr gly ala arg arg leu val
CTC AGC TCT CTG AGG CCC AGC CTG ACT GGC GCT CGG AGG CTC GTG

360
glu thr ile phe leu gly ser arg pro trp met pro gly thr pro
GAG ACC ATC TTT CTG GGT TCC AGG CCC TGG ATG CCA GGG ACT CCC

370
arg arg leu pro arg leu pro gln arg tyr trp gln met arg pro
CGC AGG TTG CCC CGC CTG CCC CAG CGC TAC TGG CAA ATG CGG CCC

380
leu phe leu glu leu leu gly asn his ala gln cys pro tyr gly
CTG TTT CTG GAG CTG CTT GGG AAC CAC GCG CAG TGC CCC TAC GGG

390
val leu leu lys thr his cys pro leu arg ala ala val thr pro
GTG CTC CTC AAG ACG CAC TGC CCG CTG CGA GCT GCG GTC ACC CCA

400
ala ala gly val cys ala arg glu lys pro gln gly ser val ala
GCA GCC GGT GTC TGT GCC CGG GAG AAG CCC CAG GGC TCT GTG GCG

410
ala pro glu glu glu asp thr asp pro arg arg leu val gln leu
GCC CCC GAG GAG GAG GAC ACA GAC CCC CGT CGC CTG GTG CAG CTG

420
leu arg gln his ser ser pro trp gln val tyr gly phe val arg
CTC CGC CAG CAC AGC AGC CCC TGG CAG GTG TAC GGC TTC GTG CGG

430
ala cys leu arg arg leu val pro pro gly leu trp gly ser arg
GCC TGC CTG CGC CGG CTG GTG CCC CCA GGC CTC TGG GGC TCC AGG

440
his asn glu arg arg phe leu arg asn thr lys lys phe ile ser
CAC AAC GAA CGC CGC TTC CTC AGG AAC ACC AAG AAG TTC ATC TCC

450
leu gly lys his ala lys leu ser leu gln glu leu thr trp lys
CTG GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACG TGG AAG

460
met ser val arg asp cys ala trp leu arg arg ser pro gly val
ATG AGC GTG CGG GAC TGC GCT TGG CTG CGC AGG AGC CCA GGG GTT

470
gly cys val pro ala ala glu his arg leu arg glu glu ile leu
GGC TGT GTT CCG GCC GCA GAG CAC CGT CTG CGT GAG GAG ATC CTG

480
520
530
540

FIG. 20C



550
 ala lys phe leu his trp leu met ser val tyr val val glu leu
 GCC AAG TTC CTG CAC TGG CTG ATG AGT GTG TAC GTC GTC GAG CTG

560
 leu arg ser phe phe tyr val thr glu thr thr phe gln lys asn
 CTC AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC

570
 arg leu phe phe tyr arg lys ser val trp ser lys leu gln ser
 AGG CTC TTT TTC TAC CGG AAG AGT GTC TGG AGC AAG TTG CAA AGC

580
 arg leu phe phe tyr arg lys ser val trp ser lys leu gln ser
 AGG CTC TTT TTC TAC CGG AAG AGT GTC TGG AGC AAG TTG CAA AGC

590
 ile gly ile arg gln his leu lys arg val gln leu arg glu leu
 ATT GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG

600
 ile gly ile arg gln his leu lys arg val gln leu arg glu leu
 ATT GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG

610
 ser glu ala glu val arg gln his arg glu ala arg pro ala leu
 TCG GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG

620
 leu thr ser arg leu arg phe ile pro lys pro asp gly leu arg
 CTG ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG

630
 leu thr ser arg leu arg phe ile pro lys pro asp gly leu arg
 CTG ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG

640
 pro ile val asn met asp tyr val val gly ala arg thr phe arg
 CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC

650
 arg glu lys arg ala glu arg leu thr ser arg val lys ala leu
 AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG

660
 arg glu lys arg ala glu arg leu thr ser arg val lys ala leu
 AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG

670
 phe ser val leu asn tyr glu arg ala arg arg pro gly leu leu
 TTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC GGC CTC CTG

680
 gly ala ser val leu gly leu asp asp ile his arg ala trp arg
 GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC

690
 gly ala ser val leu gly leu asp asp ile his arg ala trp arg
 GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC

700
 thr phe val leu arg val arg ala gln asp pro pro pro glu leu
 ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG CTG

710
 tyr phe val lys val asp val thr gly ala tyr asp thr ile pro
 TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC

720
 tyr phe val lys val asp val thr gly ala tyr asp thr ile pro
 TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC

730
 gln asp arg leu thr glu val ile ala ser ile ile lys pro gln
 CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG

740
 asn thr tyr cys val arg arg tyr ala val val gln lys ala ala
 AAC ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC

750
 asn thr tyr cys val arg arg tyr ala val val gln lys ala ala
 AAC ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC

FIG. 20D

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27/103



his gly his val arg lys ala phe lys ser his val leu arg pro
 CAT GGG CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC CTA CGT CCA

760
 val pro gly asp pro ala gly leu his pro leu his ala ala leu
 GTG CCA GGG GAT CCC GCA GGG CTC CAT CCT CTC CAC GCT GCT CTG

770
 780
 gln pro val leu arg arg his gly glu gln ala val cys gly asp
 CAG CCT GTG CTA CGG CGA CAT GGA GAA CAA GCT GTT TGC GGG GAT

790
 800
 ser ala gly arg ala ala pro ala phe gly gly OP
 TCG GCG GGA CGG GCT GCT CCT GCG TTT GGT GGA TGA TTTCTTGTGGT

807
 GACACCTCACCTCACCCACGCGAAAACTTCCTCAGGACCTGGTCCGAGGTGTCCCTGA
 GTATGGCTGCGTGGTGAACCTTGCGGAAGACAGTGGTGAACCTTCCCTGTAGAAGACGAGGC
 CCTGGGTGGCACGGCTTTTGTTCAGATGCCGGCCACGGCCTATTCCCCTGGTGCGGCCT
 GCTGCTGGATACCCGGACCTGGAGGTGCAGAGCGACTACTCCAGCTATGCCCGGACCTC
 CATCAGAGCCAGTCTCACCTTCAACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAA
 ACTCTTTGGGGTCTTGCGGCTGAAGTGTCACAGCCTGTTTCTGGATTTGCAGGTGAACAG
 CCTCCAGACGGTGTGCACCAACATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCA
 CGCATGTGTGCTGCAGTCTCCATTTTCATCAGCAAGTTTGGAAGAACCCACATTTTTCT
 GCGCGTCATCTCTGACACGGCCTCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGG
 GATGTCGCTGGGGGCCAAGGGCGCCGCCGCGCCTCTGCCCTCCGAGGCCGTGCAGTGGCT
 GTGCCACCAAGCATTCCTGCTCAAGCTGACTCGACACCGTGTCACCTACGTGCCACTCCT
 GGGGTCACTCAGGACAGCCCAGACGCAGCTGAGTCGGAAGCTCCCGGGGACGACGCTGAC
 TGCCCTGGAGGCCGAGCCAACCCGGCACTGCCCTCAGACTTCAAGACCATCCTGGACTG
 ATGGCCACCCGCCCACAGCCAGGCCGAGAGCAGACACCAGCAGCCCTGTACGCCGGGCT
 CTACGTCCCAGGGAGGGAGGGGCGGCCACACCCAGGCCCGCACCGCTGGGAGTCTGAGG
 CCTGAGTGAGTGTGTTGCGCGAGGCCTGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAG
 GCCTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTCCAGCACACCTGCCGTCTTCACTTCCC
 CACAGGCTGGCGCTCGGCTCCACCCCAGGGCCAGCTTTTCTCACCAGGAGCCCGGCTTC
 CACTCCCCACATAGGAATAGTCCATCCCCAGATTGCGCCATTGTTACCCCTCGCCCTGCC
 CTCCTTTGCCTTCCACCCCCACCATCCAGGTGGAGACCTGAGAAGGACCCCTGGGAGCTC
 TGGGAATTTGGAGTGACCAAAGGTGTGCCCTGTACACAGGCGAGGACCCTGCACCTGGAT
 GGGGGTCCCTGTGGGTCAAATTGGGGGGAGGTGCTGTGGGAGTAAAATACTGAATATATG
 AGTTTTTCAGTTTTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIG. 20E

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28/103

1 CCATGGGACCCACTGCAGGGGCAGCTGGGAGGCTGCAGGCTTCAGGTCCCAGTGGGGTTG
GGTACCCTGGGTGACGTCCCCGTCGACCTCCGACGTCCGAAGTCCAGGGTCACCCCAAC

61 CCATCTGCCAGTAGAAACCTGATGTAGAATCAGGGCGCGAGTGTGGACACTGTCTTGAAT
GGTAGACGGTCATCTTTGGACTACATCTTAGTCCCGCGCTCACACCTGTGACAGGACTTA

121 CTCAATGTCTCAGTGTGTGCTGAAACATGTAGAAATTAAAGTCCATCCCTCCTACTCTAC
GAGTTACAGAGTCACACACGACTTTGTACATCTTTAATTTAGGTAGGGAGGATGAGATG

181 TGGGATTGAGCCCCCTTCCCTATCCCCCCCCAGGGGCAGAGGAGTTCTCTCACTCCTGTG
ACCCTAACTCGGGGAAGGGATAGGGGGGGTCCCCGTCTCCTCAAGGAGAGTGAGGACAC

241 GAGGAAGGAATGATACTTTGTTATTTTTCACTGCTGGTACTGAATCCACTGTTTCATTG
CTCCTTCTTACTATGAAACAATAAAAAGTGACGACCATGACTTAGGTGACAAAGTAAAC

301 TTGGTTTGTTTGTGTTTGTGTTTGTGAGAGGCGGTTTCACTCTTGTTGCTCAGGCTGGAGGGAG
AACCACAAACAAACAAACAAACTCTCCGCCAAAGTGAGAACAACGAGTCCGACCTCCCTC

361 TGCAATGGCGGATCTTGGCTTACTGCAGCCTCTGCCTCCAGGTTCAAGTGATTCTCTCT
ACGTTACCGCGCTAGAACC GAATGACGTCGGAGACGGAGGGTCCAAGTTCACTAAGAGGA

alu

421 GCTTCCGCCTCCCATTTGGCTGGGATTACAGGCACCCGCCACCATGCCCAGCTAATTTTT
CGAAGGCGGAGGGTAAACCGACCCCTAATGTCCGTGGGCGGTGGTACGGGTCGATTAAAAA

==

481 TGTATTTTTAGTAGAGACGGGGGTGGGGGTGGGGTTCAACATGTTGGCCAGGCTGGTCTC
ACATAAAAATCATCTCTGCCCCCACCCCCACCCCAAGTGGTACAACCGGTCCGACCAGAG

CAP
===== >

541 GAACTTCTGACCTCAGATGATCCACCTGCCTCTGCCTCCTAAAGTGCTGGGATTACAGGT
CTTGAAGACTGGAGTCTACTAGGTGGACGGAGACGGAGGATTTACGACCCTAATGTCCA

601 GTGAGCCACCATGCCCAGCTCAGAATTTACTCTGTTTAGAAACATCTGGGTCTGAGGTAG
CACTCGGTGGTACGGGTGAGTCTTAAATGAGACAAATCTTTGTAGACCCAGACTCCATC

CCAAT
***** >

661 GAAGCTCACCCCACTCAAGTGTTGTGGTGTGTTTAAAGCCAATGATAGAATTTTTTTATTGT
CTTCGAGTGGGGTGAGTTCACAACACCACAAAATTCGGTTACTATCTTAAAAAATAACA

721 TGTTAGAACACTCTTGATGTTTACTGTGATGACTAAGACATCATCAGCTTTTCAAAG
ACAATCTTGAGAACTACAAAATGTGACACTACTGATTCTGTAGTAGTCGAAAAGTTTC

FIG. 21A



29/103

CAP

*****>

781 ACACACTAACTGCACCCATAATACTGGGGTGTCTTCTGGGTATCAGCGATCTTCATTGAA
TGTGTGATTGACGTGGGTATTATGACCCACAGAAGACCCATAGTCGCTAGAAGTAACTT

CAP

841 TGCCGGGAGGCGTTTCCTCGCCATGCACATGGTGTTAATTACTCCAGCATAATCTTCTGC
ACGGCCCTCCGCAAAGGAGCGGTACGTGTACCACAATTAATGAGGTTCGTATTAGAAGACG

***>

901 TTCCATTTCTTCTCTTCCCTCTTTTAAAATTGTGTTTTCTATGTTGGCTTCTCTGCAGAG
AAGGTAAAGAAGAGAAGGGAGAAAATTTTAACACAAAAGATACAACCGAAGAGACGTCTC

CAP

*****>

961 AACCAGTGTAAGCTACAACCTAACTTTTGTGGAACAAATTTTCAAACCGCCCCCTTTGC
TTGGTCACATTCGATGTTGAATTGAAACAACCTTGTTTAAAAGGTTGGCGGGGAAACG

1021 CCTAGTGGCAGAGACAATTCACAAACACAGCCCTTTAAAAAGGCTTAGGGATCACTAAGG
GGATCACCGTCTCTGTTAAGTGTGTTGTGTCGGGAAATTTTCCGAATCCCTAGTGATTCC

1081 GGATTTCTAGAAGAGCGACCCGTAATCCTTAAGTATTTACAAGACGAGGCTAACCTCCAG
CCTAAAGATCTTCTCGCTGGGCATTAGGAATTCATAAATGTTCTGCTCCGATTGGAGGTC

1141 CGAGCGTGACAGCCCAGGGAGGGTGCGAGGCCTGTTCAAATGCTAAGCTTCCATAAATAA
GCTCGCACTGTCCGGTCCCTCCACGCTCCGACAAAGTTTACGATTGGAAGGTATTTATT

1201 AGCAAATTTCCCTCCGGCAGTTTCTGGAAAGTAGGAAAGGTTAACATTTAAGGTTGCGTTT
TCGTTTAAAGGAGGCCGTCAAAGACCTTTCATCCTTTCCAATTGTAAATTTCAACGCAAA

1261 GTTAGCATTTCAAGTGTGTTGCCGACCTCAGCTAACAGCATCCCTGCAAGGCCTCGGGAGAC
CAATCGTAAAGTCACAAACGGCTGGAGTCGATTGTCGTAGGGACGTTCCGGAGCCCTCTG

1321 CCAGAAGTTTCTCGCCCCTTAGATCCAACTTGAGCAACCCGGAGTCTGGATTCTTGGGA
GGTCTTCAAAGAGCGGGGAATCTAGGTTTGAACCTCGTTGGGCCTCAGACCTAAGGACCCT

TopoII

*****>

1381 AGTCCTCAGCTGTCTGCGGTTGTGCCGGGGCCCCAGGTCTGGAGGGGACCAAGTGGCCGT
TCAGGAGTCGACAGGACGCCAACACGGCCCCGGGGTCCAGACCTCCCCTGGTCACCGGCA

1441 GTGGCTTCTACTGCTGGGCTGGAAGTCGGGCCTCCTAGCTCTGCAGTCCGAGGCTTGGAG
CACCGAAGATGACGACCCGACCTTCAGCCCGGAGGATCGAGACGTCAGGCTCCGAACCTC

1501 CCAGGTGCCTGGACCCCGAGGCTGCCCTCCACCCTGTGCGGGCGGGATGTGACCAGATGT
GGTCCACGGACCTGGGGCTCCGACGGGAGGTGGGACACGCCCGCCCTACACTGGTCTACA

1561 TGGCCTCATCTGCCAGACAGAGTGCCGGGGCCCAGGGTCAAGGCCGTTGTGGCTGGTGTG
ACCGGAGTAGACGGTCTGTCTACGGCCCCGGGTCCAGTTCCGGCAACACCGACCACAC

1621 AGGCGCCCGGTGCGCGGCCAGCAGGAGCGCCTGGCTCCATTTCCACCCCTTCTCGACGG
TCCGCGGGCCACGCGCCGGTCTGCTCGCGGACCGAGGTAAAGGTGGGAAAGAGCTGCC

FIG. 21B



30/103

1681 GACCGCCCCGGTGGGTGATTAACAGATATTGGGGTGGTTTGCTCATGGTGGGGACCCCTT
CTGGCGGGGCCACCCACTAATTGTCTATAACCCCAACAAACGAGTACCACCCCTGGGGAA
1741 CGCCGCCTGAGAACCTGCAAAGAGAAATGACGGGCCTGTGTCAAGGAGCCCAAGTCGCGG
GCGGCGGACTCTTGACGTTTCTCTTTACTGCCCGGACACAGTTCTCGGGTTCAGCGCC
1801 GGAAGTGTTCAGGGAGGCACTCCGGGAGGTCCCGCGTCCCCGTCCAGGGAGCAATGCGT
CCTTCACAACGTCCCTCCGTGAGGCCCTCCAGGGCGCACGGGCAGGTCCCTCGTTACGCA
1861 CCTCGGGTTCGTCCCCAGCCGCGTCTACGCGCCTCCGTCTCCCTTCACGTCCGGCATT
GGAGCCCAAGCAGGGGTGCGCGCAGATGCGCGGAGGCAGGAGGGGAAGTGCAGGCCGTAA
1921 CGTGGTGCCCGGAGCCCGACGCCCCGCGTCCGGACCTGGAGGCAGCCCTGGGTCTCCGGA
GCACCACGGGCCTCGGGCTGCGGGGCGCAGGCCTGGACCTCCGTCCGGACCCAGAGGCCT
1981 TCAGGCCAGCGGCCAAAGGGTCGCCGACGACCTGTTCCAGGGCCTCCACATCATGGC
AGTCCGGTCGCCGGTTTCCAGCGGCGTGCCTGGACAAGGGTCCCGGAGGTGTAGTACCG
2041 CCCTCCCTCGGGTTACCCACAGCCTAGGCCGATTGACCTCTCTCCGTGGGGCCCTCG
GGGAGGGAGCCCAATGGGGTGTGCGATCCGGCTAAGCTGGAGAGAGGCGACCCCGGGAGC

Sp1

2101 CTGGCGTCCCTGCACCTGGGAGCGCGAGCGGCGCGCGGGCGGGGAAGCGCGGCCAGAC
GACCGCAGGGACGTGGGACCCCTCGCGCTCGCCGCGCGCCCCGCCCTTCGCGCCGGGTCTG
2161 CCCCCGGTCCGCGCGGAGCAGCTGCGCTGTGCGGGCCAGGCCGGGTCCAGTGGATTCTG
GGGGCCAGGCGGGCCTCGTCGACGCGACAGCCCCGGTCCGGCCGAGGGTCACTAAGC
2221 CGGGCAACAGACGCCCAGGACCGCGCTTCCACGTGGCGGAGGGACTGGGGACCCGGGCA
GCCCCGTTGTCTGCGGGTCTTGCGCGGAAGGGTGCACCGCCTCCCTGACCCCTGGGGCCGT

Sp1

=====

E2F

2281 CCGGTCCTGCCCCCTTACCTTCCAGCTCCGCCTCGTCCGCGCGGAACCCGCCCCGTCCC
GGCCAGGACGGGGAAGTGGAAGGTGAGGCGGAGCAGGCGCGCCTTGGGGCGGGGCAGGG
2341 GAACCTTTCGGGTCCCCGGGCCAGCCCCCTTCCGGGCCATCCCAGCCCGTCCCGTTCTT
CTTGGAAGGGCCAGGGGCCGGTTCGGGAAGGCCCGGTAGGGTCGGGCAGGGCAAGGA

Sp1

=====

E2F

NFkB

2401 TTTCCGCGGCCCCGCCCTCTCCTCGCGGCGCGAGTTTCAGGCAGCGCTGCGTCTGCTGC
AAAGGCGCCGGGGCGGGAGAGGAGCGCCGCGCTCAAAGTCCGTGCGACGCAGGACGACG

hTRT5'

*****>

2461 GCACGTGGGAAGCCCTGGCCCCGGCCACCCCGCGATGCCGCGCGTCCCCGCTGCCGAG
CGTGCAACCTTCGGGACCGGGGCCGGTGGGGGCGCTACGGCGCGGAGGGGCGACGGCTC
2521 CCGTGCGTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTCTGTC
GGCAGCGAGGGACGACGCGTCCGTGATGGCGCTCCACGACGGCGACCGGTGCAAGCACG

FIG. 21C



31/103

E2F

2581 GGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGGGACCCGGCGGCTTTCCGCG
CCGCGGACCCCGGGGTCCCAGACCGCCGACCACGTGCGGCCCTGGGCCGCCGAAAGGCGC

*

2641 CGCTGGTGGCCAGTGCTTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCGCGCCC
GCGACCACCGGGTCACGGACCACACGCACGGGACCCTGCGTGCCGGCGGGGGGCGGCGGG

NFkB

=====

2701 CCTCCTTCCGCCAGGTGGGCTCCCCGGGGTCCGCGTCCGGCTGGGGTTGAGGGCGGCGC
GGAGGAAGGCGGTCCACCCGAGGGGCCAGCCGACGGCCGACCCCAACTCCCGCCGGC

Topo_II_cleavag

::::::::::::::

NFkB

+++++++

NFkB

=====

Intron1

*****>

2761 GGGGAACCGAGCGACATGCGGAGAGCAGCGCAGGCGACTCAGGGCGCTTCCCCCGAGGT
CCCCCTTGGTCGCTGTACGCTCTCGTCGCGTCCGCTGAGTCCCGCGAAGGGGGCGTCCA

e_site

::::

2821 GTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAA
CAGGACGGACTTCCTCGACCACCGGGCTCACGACGTCTCCGACACGCTCGCGCCGCGCTT

2881 GAACGTGCTGGCCTTCGGCTTCGCGTGCTGGACGGGGCCCGCGGGGGCCCCCGAGGC
CTTGCACGACCGGAAGCCGAAGCGCGACGACCTGCCCGGGCGCCCCCGGGGGGCTCCG

2941 CTTCAACCACGCGTGCGCAGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAG
GAAGTGGTGGTTCGACGCGTCGATGGACGGGTGTGCCACTGGCTGCGTGACGCCCCCTC

3001 CGGGGCGTGGGGGCTGCTGCTGCGCCGCGTGGGCGACGACGTGCTGGTTACCTGCTGGC
GCCCCGACCCCCGACGACGACGCGGCGCACCCGCTGCTGCACGACCAAGTGGACGACCG

3061 ACGCTGCGCGCTCTTTGTGCTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCC
TGCGACGCGCGAGAAACAGACCACCGAGGGTCGACGCGGATGGTCCACAGCCCCGCGG

3121 GCTGTACCAGCTCGGCGCTGCCACTCAGGCCCGGCCCCCGCCACACGCTAGTGGAACCCG
CGACATGGTCGAGCCGCGACGGTGAGTCCGGGCGGGGGCGGTGTGCGATCACCTGGGGC

3181 AAGGCGTCTGGGATGCGAACGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCT
TTCCGACGACCCCTACGCTTGCCCCGACCTTGGTATCGCAGTCCCTCCGGCCCCAGGGGA

3241 GGGCCTGCCAGCCCCGGGTGCGAGGAGGCGGGGGCAGTGCCAGCCGAAGTCTGCCGTT
CCCGACGGTCGGGGCCACGCTCCTCCGCGCCCCCGTCACGGTCGGCTTCAGACGGCAA

3301 GCCCAAGAGGCCAGGCGTGGCGCTGCCCCTGAGCCGGAGCGGACGCCCCGTTGGGCAGGG
CGGGTTCTCCGGGTCCGCACCGCGACGGGACTCGGCCTCGCCTGCGGGCAACCCGTCCC

FIG. 21D



32/103

3361 GTCCTGGGCCCCACCCGGGCAGGACGCGTGACCGAGTGACCGTGGTTTCTGTGTGGTGTC
CAGGACCCGGGTGGGCCCCGTCCTGCGCACCTGGCTCACTGGCACCAAAGACACACCACAG

3421 ACCTGCCAGACCCGCCGAAGAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCA
TGGACGGTCTGGGCGGCTTCTTCGGTGGAGAAACCTCCACGCGAGAGACCGTGCGCGGT

3481 CTCCCACCCATCCGTGGGCCGCCAGCACACGCGGGCCCCCATCCACATCGCGGCCACC
GAGGGTGGGTAGGCACCCGGCGGTCTGTGGTGCGCCCGGGGGGTAGGTGTAGCGCCGGTGG

3541 ACGTCCCTGGGACACGCCTTGTCCCCCGGTGTACGCCGAGACCAAGCACTTCTCTACTC
TGCAGGGACCTGTGCGGAACAGGGGGCCACATGCGGCTCTGGTTCGTGAAGGAGATGAG

3601 CTCAGGCGACAAGGAGCAGCTGCGGCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCT
GAGTCCGCTGTTCTCTCGTCGACGCCGGGAGGAAGGATGAGTCGAGAGACTCCGGGTCCGA

3661 GACTGGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCAGGCCCCTGGATGCCAGG
CTGACCGCGAGCCTCCGAGCACCTCTGGTAGAAAGACCCAAGGTCCGGGACCTACGGTCC

3721 GACTCCCCGCAGGTTGCCCCGCCTGCCCCAGCGCTACTGGCAAATGCGGGCCCTGTTTCT
CTGAGGGGCGTCCAACGGGGCGGACGGGGTTCGCGATGACCGTTTACGCCGGGGACAAAGA

3781 GGAGCTGCTTGGGAACCACGCGCAGTGCCCCCTACGGGGTGCTCCTCAAGACGCACTGCCC
CCTCGACGAACCCTTGGTGCGGTCACGGGGATGCCCCACGAGGAGTTCTGCGTGACGGG

3841 GCTGCGAGCTGCGGTCACCCCAGCAGCCGGTGTCTGTGCCCGGGAGAAGCCCCAGGGCTC
CGACGCTCGACGCCAGTGGGGTCGTGCGCCACAGACACGGGCCCTCTTCGGGGTCCCCGAG

3901 TGTGGCGGCCCCCGAGGAGGAGGACACAGACCCCCGTGCGCTGGTGCAGCTGCTCCGCCA
ACACCGCCGGGGGCTCCTCCTCCTGTGTCTGGGGGACGCGGACCACGTGACGAGGCGGT

3961 GCACAGCAGCCCCTGGCAGGTGTACGGCTTCGTGCGGGCCTGCTGCGCCGGCTGGTGGC
CGTGTCTGTCGGGGACCGTCCACATGCCGAAGCACGCCCGGACGGACGCGGCCGACCACGG

4021 CCCAGGCCTCTGGGGCTCCAGGCACAACGAACGCCGCTTCTCAGGAACACCAAGAAGTT
GGGTCCGGAGACCCCGAGGTCCGTGTTGCTTGCGGCGAAGGAGTCCTTGTGGTTCTTCAA

4081 CATCTCCCTGGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGT
GTAGAGGGACCCCTTCGTACGGTTCGAGAGCGACGTCTCGACTGCACCTTCTACTCGCA

4141 GCGGGACTGCGCTTGGCTGCGCAGGAGCCCAGGTGAGGAGGTGGTGGCCGTCGAGGGCCC
CGCCCTGACGCGAACCGACGCGTCCCTCGGGTCCACTCCTCCACCACCGGCAGCTCCCGGG

Intron2

4201 AGGCCCCAGAGCTGAATGCAGTAGGGGCTCAGAAAAGGGGGCAGGCAGAGCCCTGGTCT
TCCGGGGTCTCGACTTACGTACATCCCCGAGTCTTTTCCCCCGTCCGTCTCGGGACCAGGA

4261 CCTGTCTCCATCGTCACGTGGGCACACGTGGCTTTTCGCTCAGGACGTGAGTGGACACG
GGACAGAGGTAGCAGTGACCCGTGTGCACCGAAAAGCGAGTCCTGCAGCTCACCTGTGC

*****>

4321 GTGATCGAGGTCGAC
CACTAGCTCCAGCTG

FIG. 21E



33/103

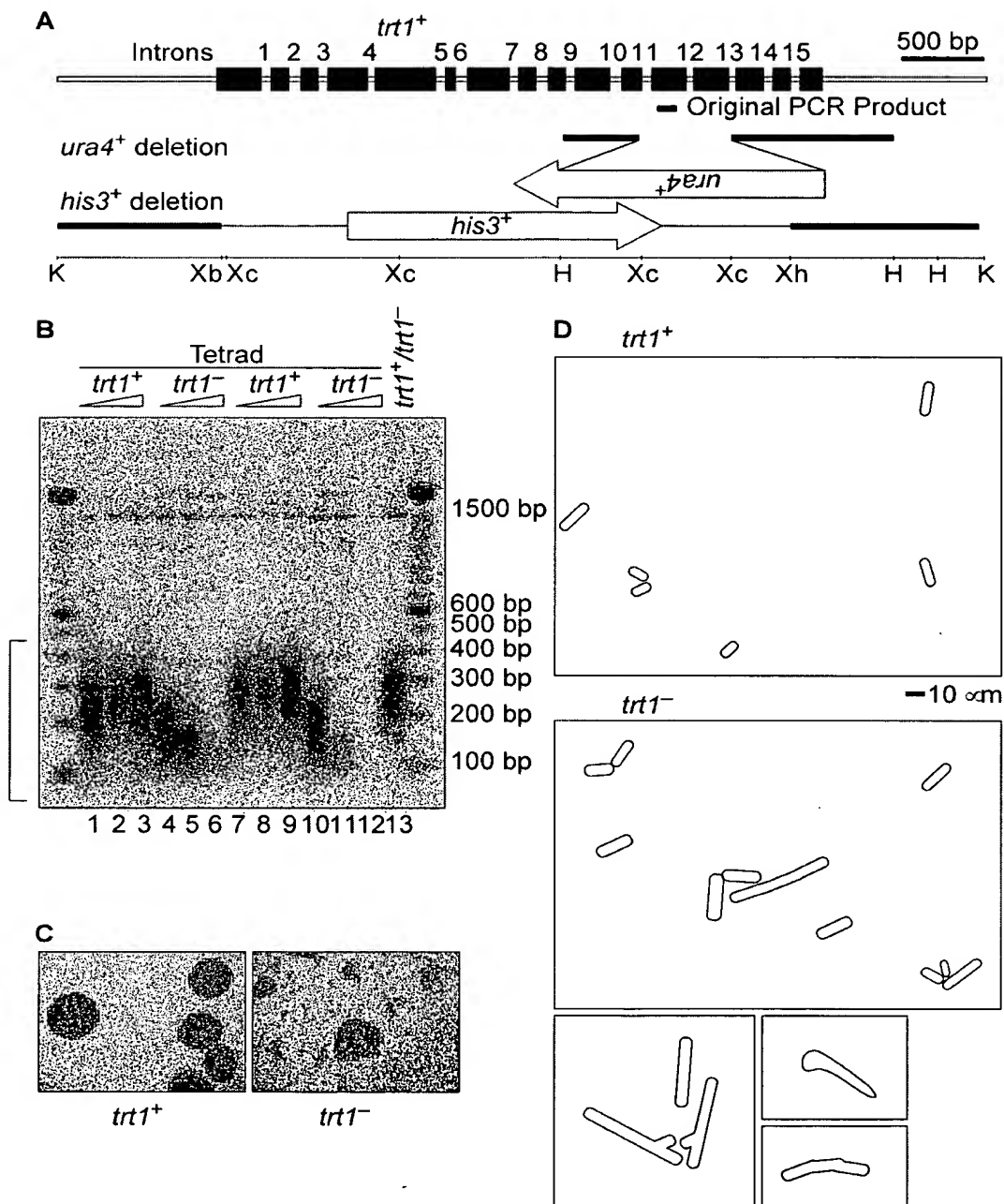


FIG. 22

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34/103



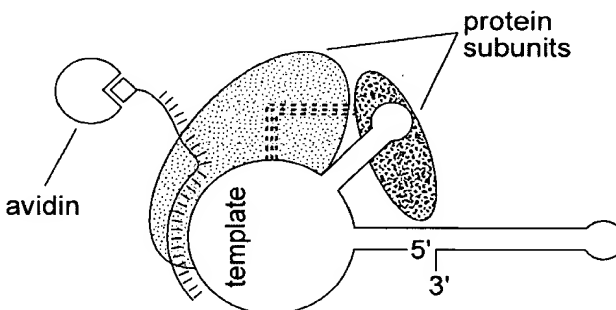
gccaagttcctgcactggctgatgagtgtgtacgtcgtcgagctgctcaggtctttcttt
 tatgtcacggagaccacgtttcaaaagaacaggtctttttctaccggaagagtgtctgg
 agcaagttgcaaagcattggaatcacagcagcacttgaagaggggtgcagctgcgggacgtg
 tcggaagcagaggtcagggcagcatcggaagccaggcccgccctgctgacgtccagactc
 cgcttcatccccaaagcctgacgggctgcggccgattgtgaacatggactacgtcgtggga
 gccagaacgttccgcagagaaaagaggccgagcgtctcacctcgaggggtgaaggcactg
 ttcagcgtgctcaactacgagcgggcgcg

FIG. 23

TCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAG
 ACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCC
 AGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATC
 AGGGGCAAGTC

FIG. 24

PANEL A



PANEL B

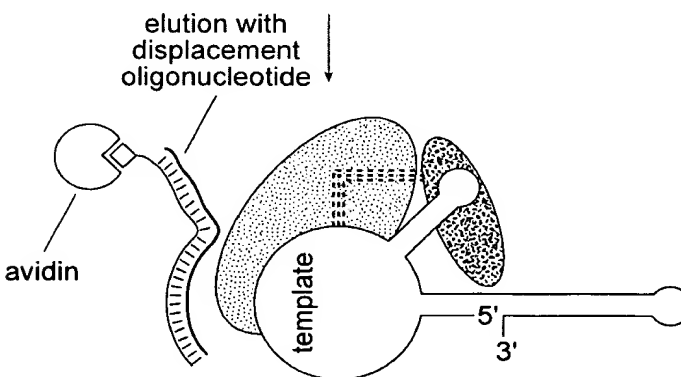


FIG. 26

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35/103

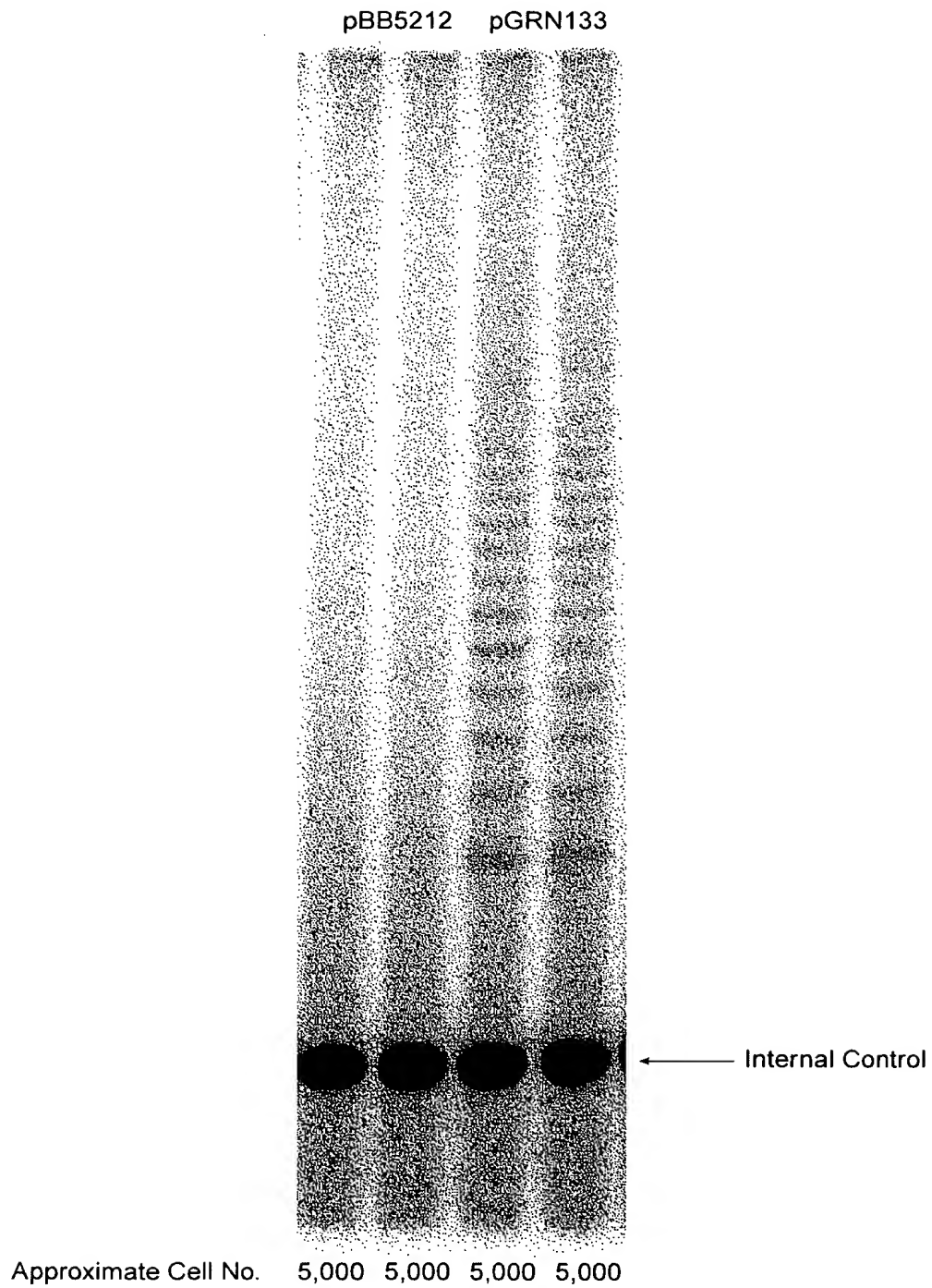


FIG. 25

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36/103

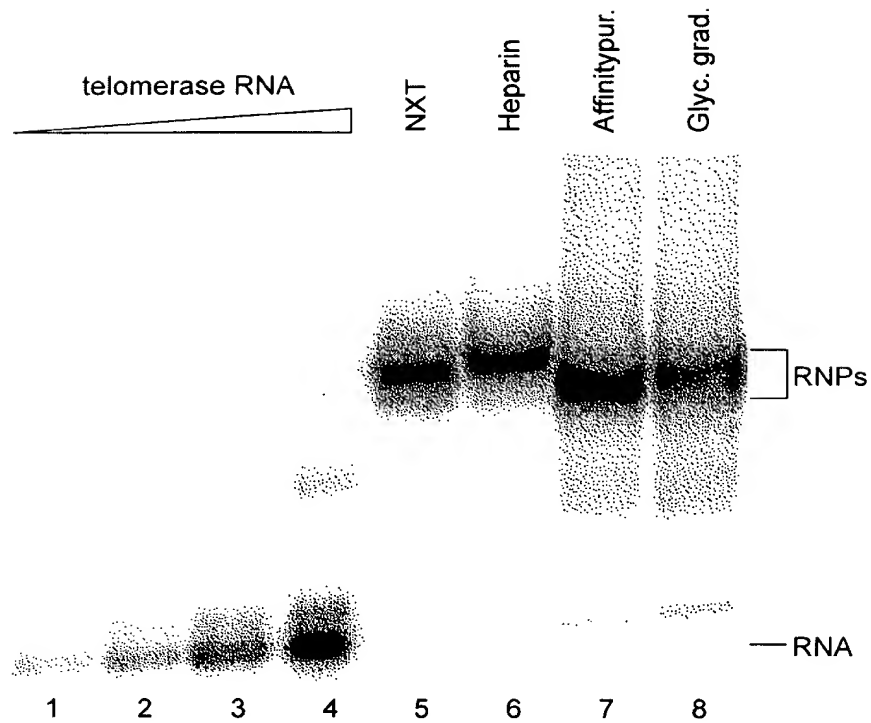


FIG. 27

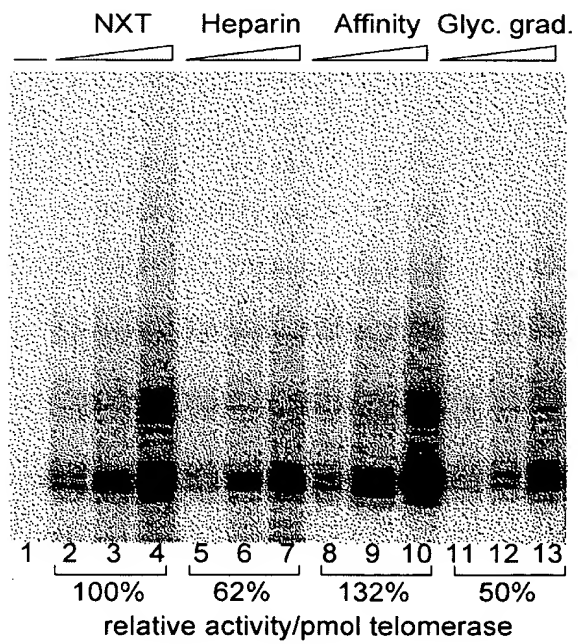


FIG. 28

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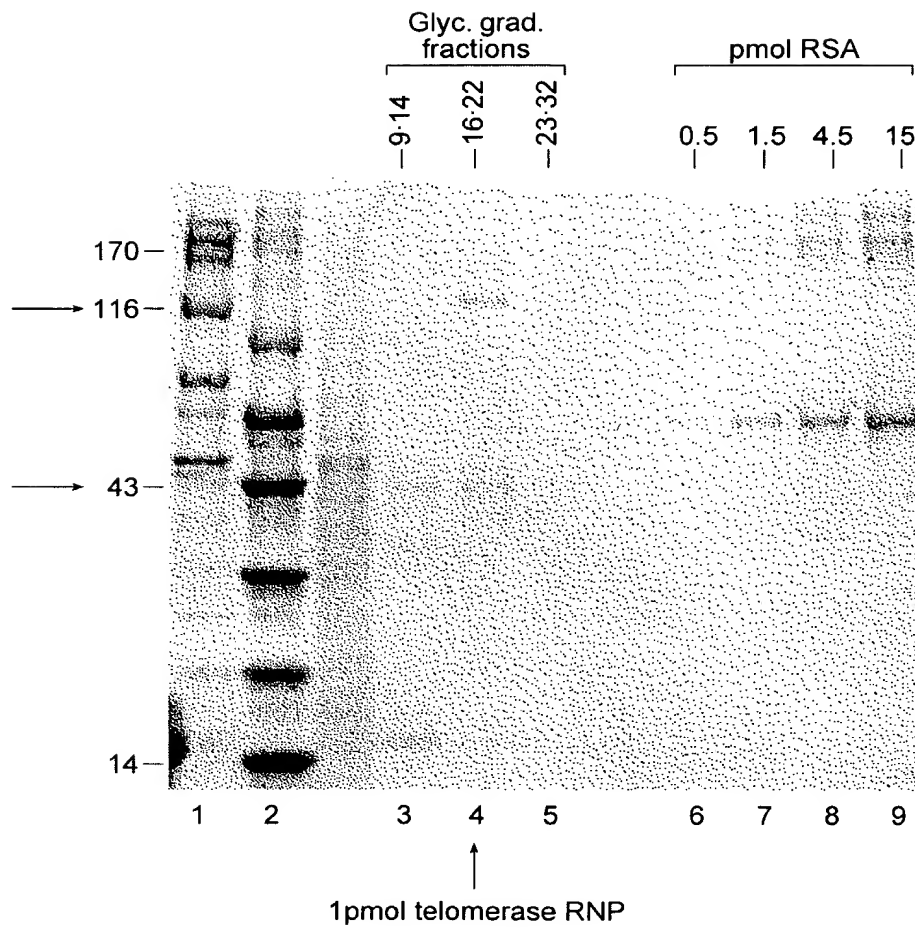


FIG. 29

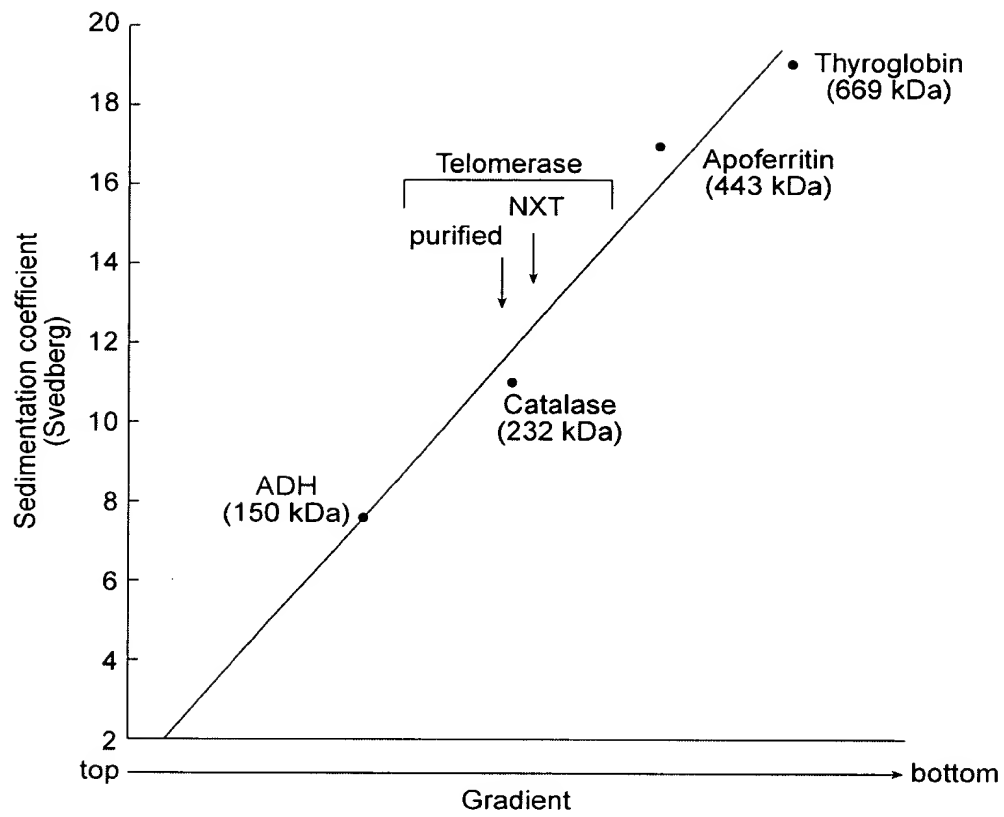


FIG. 30



Telomerase:

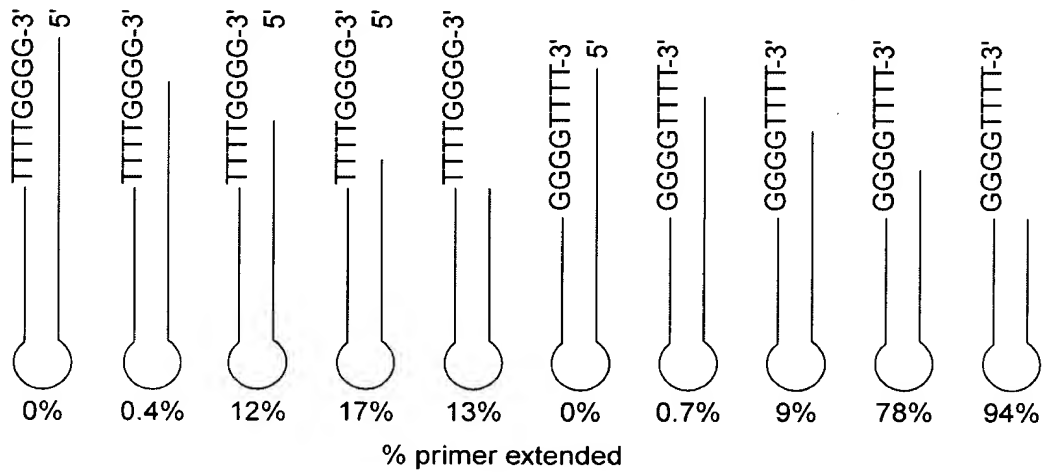
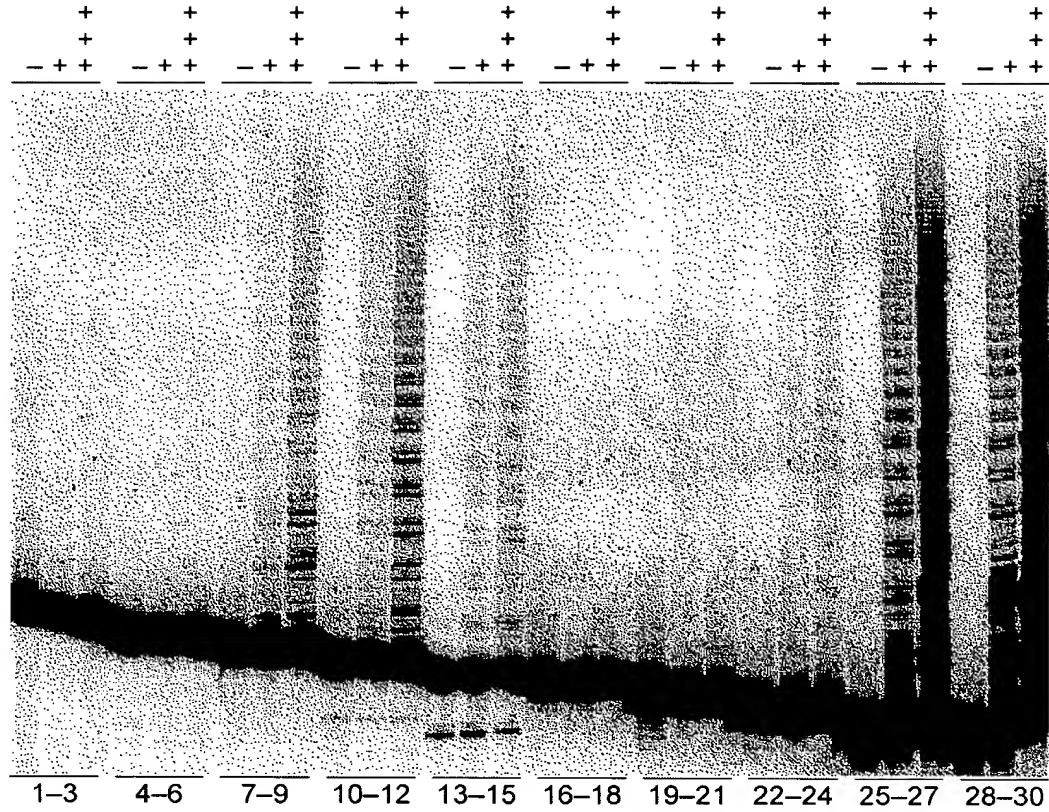


FIG. 31

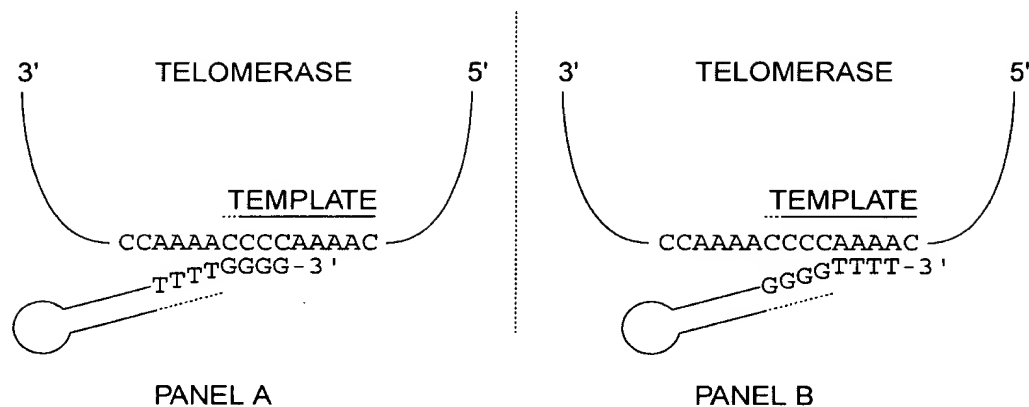


FIG. 32

1	CCCCAAAACC	CCAAAACCCC	AAAACCCCTA	TAAAAAAAGA	AAAAATTGAG
51	GTAGTTTAGA	AATAAAATAT	TATTCCTGCA	CAAATGGAGA	TGGATATTGA
101	TTTGGGATGAT	ATAGAAAATT	TACTTCCTAA	TACATTCAAC	AAGTATAGCA
151	GCTCTTGATAG	TGACAAAGAAA	GGATGCAGAAA	CATTGAAATC	TGGCTCGAAA
201	TCGCCTTCAT	TGACTATTCC	AAAGTTGCAA	AAACAATTAG	AGTTCTACTT
251	CTCGGATGCA	AATCTTTATA	ACGATTCTTT	CTTGAGAAAA	TTAGTTTTAA
301	AAAGCGGAGA	GCAAAGAGTA	GAAATTGAAA	CATTACTAAT	GTTTAAATAA
351	AATCAGGTAA	TGAGGATTAT	TCTATTTTTT	AGATCACTTC	TTAAGGAGCA
401	TTATGGAGAA	AATTACTTAA	TACTAAAAGG	TAAACAGTTT	GGATTATTTT
451	CCTAGCCAAC	AATGATGAGT	ATATTAAATT	CATATGAGAA	TGAGTCAAAG
501	GATCTCGATA	CATCAGACTT	ACCAAAGACA	AACTCGCTAT	AAAACGCAAG
551	AAAAAGTTTG	ATAATCGAAC	AGCAGAAGAA	CTTATTGCAT	TTACTATTTC
601	TATGGGTTTT	ATTACAATTG	TTTTAGGTAT	CGACGGTGAA	CTCCCGAGTC
651	TTGAGACAAT	TGAAAAAGCT	GTTTACAAC	GAAGGAATCG	CAGTTCTGAA
701	AGTTCTGATG	TGTATGCCAT	TATTTTGTGA	ATTAATCTCA	AATATCTTAT
751	CTCAATTTAA	TGGATAGCTA	TAGAAACAAA	CCAAATAAAC	CATGCAAGTT
801	TAATGGAATA	TACGTAAAT	CCTTTGGGAC	AAATGCACAC	TGAATTTATA
851	TTGGATTCTT	AAAGCATAGA	TACACAGAAT	GCTTTAGAGA	CTGATTTAGC
901	TTACAACAGA	TTACCTGTTT	TGATTACTCT	TGCTCATCTC	TTATATCTTT
951	AAAAGAAGCA	GGCGAAATGA	AAAGAAGACT	AAAGAAAGAG	ATTTCAAAAT
1001	TTGTTGATTC	TTCTGTAACC	GGAATTAACA	ACAAGAATAT	TAGCAACGAA
1051	AAAGAAGAAG	AGCTATCACA	ATCCTGATTC	TTAAAGATTT	CAAAAATTCC
1101	AGGTAAGAGA	GATACATTCA	TTAAAATTCA	TATATTATAG	TTTTTTCATTT
1151	CACAGCTGTT	ATTTTCTTTT	ATCTTAACAA	TATTTTTTGA	TTAGCTGGAA
1201	GTAAAAAGTA	TCAAATAAGA	GAAGCGCTAG	ACTGAGGTAA	CTTAGCTTAT
1251	TCACATTCAT	AGATCGACCT	TCATATATCC	AATACGATGA	TAAGGAAACA
1301	GCACTCATCC	GTTTTAAAAA	TAGTGCTATG	AGGACTAAAT	TTTTAGAGTC
1351	AAGAAATGGA	GCCGAAATCT	TAATCAAAAA	GAATTGCGTC	GATATTGCAA
1401	AAGAAATCGAA	CTCTAAATCT	TTCTGTTAATA	AGTATTACCA	ATCTTGATTG
1451	ATTGAAGAGA	TTGACGAGGC	AACTGCACAG	AAGATCATT	AAGAAATAAA
1501	GTAACCTTTA	TTAATTAGAG	AATAAACTAA	ATTACTAATA	TAGAGATCAG
1551	CGATCTTCAA	TTGACGAAAT	AAAAGCTGAA	CTAAAGTTAG	ACAATAAAAA
1601	ATACAAACCT	TGGTCAAAAT	ATTGAGGAAG	GAAAAGAAGA	CCAGTTAGCA
1651	AAAGAAAAAA	TAAGGCAATA	AATAAAATGA	GTACAGAAGT	GAAGAAATAA
1701	AAGATTTATT	TTTTTCAATA	ATTTATTGAA	AAGAGGGGTT	TTGGGGTTTT
1751	GGGGTTTTTG	GG			

FIG. 34

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41/103

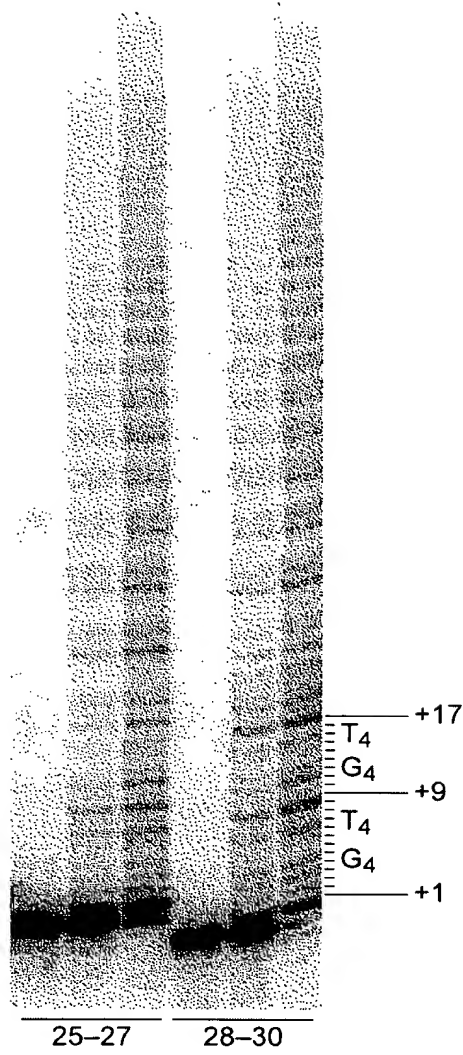


FIG. 33

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42/103

CCCCAAAACCCCAAAACCCCAAAACCCCTATAAAAAAGAAAAAATTGAGGTAGTTTAGA
1 -----+-----+-----+-----+-----+-----+-----+ 60
GGGGTTTTGGGGTTTTGGGGTTTTGGGGATATTTTTTTCTTTTTTTAACTCCATCAAATCT

a P Q N P K T P K P L * K K K K L R * F R -
b P K T P K P Q N P Y K K R K N C G S L E -
c P K P Q N P K T P I K K E K I E V V * K -

AATAAAATATTATTCCCGCACAAATGGAGATGGATATTGATTGGATGATATAGAAAATT
61 -----+-----+-----+-----+-----+-----+ 120
TTATTTTATAATAAGGGCGTGTACCTCTACCTATAACTAAACCTACTATATCTTTTAA

a N K I L F P H K W R W I L I W M I * K I -
b I K Y Y S R T N G D G Y C F G C Y R K F -
c * N I I P A Q M E M D I D L D D I E N L -

TACTTCCTAATACATTCAACAAGTATAGCAGCTCTTGTAGTGACAAGAAAGGATGCAAAA
121 -----+-----+-----+-----+-----+-----+ 180
ATGAAGGATTATGTAAGTTGTTTCATATCGTCGAGAACATCACTGTTCTTTCCTACGTTTT

a Y F L I H S T S I A A L V V T R K D A K -
b T S * Y I Q Q V * Q L L * C Q E R M Q N -
c L P N T F N K Y S S S C S D K K G C K T -

CATTGAAATCTGGCTCGAAATCGCCTTCATTGACTATTCCAAAGTTGCAAAAACAATTAG
181 -----+-----+-----+-----+-----+-----+ 240
GTAACCTTTAGACCGAGCTTTAGCGGAAGTAAGTAAAGGTTTCAACGTTTTTGTAAATC

a H C N L A R N R L H C L F Q S C K N N * -
b I E I W L E I A F I D Y S K V A K T I R -
c L K S G S K S P S L T I P K L Q K Q L E -

AGTTCTACTTCTCGGATGCAAATCTTTATAACGATTCTTTCTTGAGAAAATTAGTTTTAA
241 -----+-----+-----+-----+-----+-----+ 300
TCAAGATGAAGAGCCTACGTTTAGAAATATTGCTAAGAAAGAACTCTTTTAATCAAATTT

a S S T S R M Q I F I T I L S C E N * F * -
b V L L L G C K S L * R F F L E K I S F K -
c F Y F S D A N L Y N D S F L R K L V L K -

AAAGCGGAGAGCAAAGAGTAGAAATTGAAACATTACTAATGTTTAAATAAAATCAGGTAA
301 -----+-----+-----+-----+-----+-----+ 360
TTTCGCCTCTCGTTTCTCATCTTTAACTTTGTAATGATTACAAATTTATTTTAGTCCATT

a K A E S K E * K L K H Y * C L N K I R * -
b K R R A K S R N C N I T N V * I K S G N -
c S G E Q R V E I E T L L M F K * N Q V M -

TGAGGATTATTCTATTTTTTAGATCACTTCTTAAGGAGCATTATGGAGAAAATTACTTAA
361 -----+-----+-----+-----+-----+-----+ 420
ACTCCTAATAAGATAAAAAATCTAGTGAAGAATTCCTCGTAATACCTCTTTTAATGAATT

a C G L F Y F L D H F L R S I M E K I T * -
b E D Y S I F * I T S * G A L W R K L L N -
c R I I L F F R S L L K E H Y G E N Y L I -

FIG. 35A



43/103

421 TACTAAAAGGTAAACAGTTTGGATTATTTCCCTAGCCAACAATGATGAGTATATTAAATT 480
ATGATTTTTCATTTGTCAAACCTAATAAAGGGATCGGTTGTTACTACTCATATAATTTAA
a Y * K V N S L D Y F P S Q Q C C V Y * I -
b T K R * T V W I I S L A N N D E Y I K F -
c L K G K Q F G L F P * P T M M S I L N S -
CATATGAGAATGAGTCAAAGGATCTCGATACATCAGACTTACCAAAGACAAACTCGCTAT
481 -----+-----+-----+-----+-----+ 540
GTATACTCTTACTCAGTTTCCTAGAGCTATGTAGTCTGAATGGTTTCTGTTTGAGCGATA
a H M R M S Q R I S I H Q T Y Q R Q T R Y -
b I C E C V K G S R Y I R L T K D K L A I -
c Y E N E S K D L D T S D L P K T N S L * -
AAAACGCAAGAAAAAGTTTGATAATCGAACAGCAGAAGAACTTATTGCATTTACTATTTCG
541 -----+-----+-----+-----+-----+ 600
TTTTGCGTTCTTTTTCAAACATTAGCTTGTCTCTTCTGAATAACGTAAATGATAAGC
a K T Q E K V C * S N S R R T Y C I Y Y S -
b K R K K K F D N R T A E E L I A F T I R -
c N A R K S L I I E Q Q K N L L H L L F V -
TATGGGTTTTATTACAATTGTTTTAGGTATCGACGGTGAACCTCCCGAGTCTTGAGACAAT
601 -----+-----+-----+-----+-----+ 660
ATACCCAAAATAATGTTAACAAAATCCATAGCTGCCACTTGAGGGCTCAGAACTCTGTTA
a Y G F Y Y N C F R Y R R C T P E S C D N -
b M G F I T I V L G I D G E L P S L E T I -
c W V L L Q L F * V S T V N S R V L R Q L -
TGAAAAAGCTGTTTACAACCTGAAGGAATCGCAGTTCTGAAAAGTTCTGATGTGTATGCCAT
661 -----+-----+-----+-----+-----+ 720
ACTTTTTTCGACAAATGTTGACTTCTTAGCGTCAAGACTTTCAAGACTACACATACGGTA
a C K S C L Q L K E S Q F C K F C C V C H -
b E K A V Y N C R N R S S E S S D V Y A I -
c K K L F T T E G I A V L K V L M C M P L -
TATTTTGTGAATTAATCTCAAATATCTTATCTCAATTTAATGGATAGCTATAGAAACAAA
721 -----+-----+-----+-----+-----+ 780
ATAAAACACTTAATTAGAGTTTATAGAATAGAGTTAAATTACCTATCGATATCTTTGTTT
a Y F V N * S Q I S Y L N L M D S Y R N K -
b I L C I N L K Y L I S I * W I A I E T N -
c F C E L I S N I L S Q F N G * L * K Q T -
CCAAATAAACCATGCAAGTTTAAATGGAATATACGTTAAATCCTTTGGGACAAATGCACAC
781 -----+-----+-----+-----+-----+ 840
GGTTTATTTGGTACGTTCAAATTACCTTATATGCAATTTAGGAAACCCTGTTTACGTGTG
a P N K P C K F N G I Y V K S F G T N A H -
b Q I N H A S L M E Y T L N P L G Q M H T -
c K * T M Q V * W N I R * I L W D K C T L -
TGAATTTTATATTGGATTCTTAAAGCATAGATACACAGAATGCTTTAGAGACTGATTTAGC
841 -----+-----+-----+-----+-----+ 900
ACTTAAATATAACCTAAGAATTCGTATCTATGTGTCTTACGAAATCTCTGACTAAATCG
a C I Y I G F L K H R Y T E C F R D C F S -
b E F I L D S * S I D T Q N A L E T D L A -
c N L Y W I L K A * I H R M L * R L I * L -

FIG. 35B



44/103

TTACAACAGATTACCTGTTTTGATTACTCTTGCTCATCTCTTATATCTTTAAAAGAAGCA
901 -----+-----+-----+-----+-----+ 960
AATGTTGTCTAATGGACAAACTAATGAGAACGAGTAGAGAATATAGAAATTTTCTTCGT

a L Q Q I T C F D Y S C S S L I S L K E A -
b Y N R L P V L I T L A H L L Y L * K K Q -
c T T D Y L F C L L L L I S Y I F K R S R -

GGCGAAATGAAAAGAAGACTAAAGAAAGAGATTTCAAATTTGTTGATTCTTCTGTAACC
961 -----+-----+-----+-----+-----+ 1020
CCGCTTTACTTTTCTTCTGATTTCTTTCTCTAAAGTTTTAAACAACATAAGAAGACATTGG

a G E M K R R L K K E I S K F V D S S V T -
b A K C K E D * R K R F Q N L L I L L * P -
c R N E K K T K E R D F K I C C F F C N R -

GGAATTAACAACAAGAATATTAGCAACGAAAAAGAAGAGCTATCACAATCCTGATTC
1021 -----+-----+-----+-----+-----+ 1080
CCTTAATTGTTGTTCTTATAATCGTTGCTTTTTCTTCTCTCGATAGTGTAGGACTAAG

a G I N N K N I S N E K E E E L S Q S C F -
b E L T T R I L A T K K K K S Y H N P D S -
c N * Q Q E Y * Q R K R R R A I T I L I L -

TTAAAGATTTCAAAAATTCAGGTAAGAGAGATACATTCATTAAAATTCATATATTATAG
1081 -----+-----+-----+-----+-----+ 1140
AATTTCTAAAGTTTTTAAGGTCCATTCTCTCTATGTAAGTAATTTTAAGTATATAATATC

a L K I S K I P G K R D T F I K I H I L * -
b * R F Q K F Q V R E I H S L K F I Y Y S -
c K D F K N S R * E R Y I H * N S Y I I V -

TTTTTCATTTACAGCTGTTATTTTCTTTTATCTTAACAATATTTTTTGATTAGCTGGAA
1141 -----+-----+-----+-----+-----+ 1200
AAAAAGTAAAGTGTGACATAAAAGAAAATAGAATTGTTATAAAAACTAATCGACCTT

a F F I S Q L L F S F I L T I F F D * L E -
b F S F H S C Y F L L S * Q Y F L I S W K -
c F H F T A V I F F Y L N N I F C L A G S -

GTA AAAAGTATCAAATAAGAGAAGCGCTAGACTGAGGTAACCTAGCTTATTCACATTCAT
1201 -----+-----+-----+-----+-----+ 1260
CATTTTTTCATAGTTTATTCTCTTCGCGATCTGACTCCATTGAATCGAATAAGTGTAAGTA

a V K S I K * E K R * T E V T * L I H I H -
b * K V S N K R S A R L R * L S L F T F I -
c K K Y Q I R E A L D C G N L A Y S H S * -

AGATCGACCTTCATATATCCAATACGATGATAAGGAAACAGCAGTCATCCGTTTTAAAAA
1261 -----+-----+-----+-----+-----+ 1320
TCTAGCTGGAAGTATATAGGTTATGCTACTATTCTTTGTCGTCAGTAGGCAAAATTTT

a R S T F I Y P I R C * G N S S H P F * K -
b D R P S Y I Q Y D D K E T A V I R F K N -
c I D L H I S N T M I R K Q Q S S V L K I -

TAGTGCTATGAGGACTAAATTTTTAGAGTCAAGAAATGGAGCCGAAATCTTAATCAAAAA
1321 -----+-----+-----+-----+-----+ 1380
ATCACGATACTCCTGATTTAAAAATCTCAGTTCTTTACCTCGGCTTTAGAATTAGTTTTT

a * C Y E D * I F R V K K W S R N L N Q K -
b S A M R T K F L E S R N G A E I L I K K -
c V L C G L N F * S Q E M E P K S * S K R -

FIG. 35C



45/103

GAATTGCGTCGATATTGCAAAAGAATCGAACTCTAAATCTTTTCGTTAATAAGTATTACCA
1381 -----+-----+-----+-----+-----+-----+ 1440
CTTAACGCAGCTATAACGTTTTCTTAGCTTGAGATTTAGAAAGCAATTATTCATAATGGT

a E L R R Y C K R I E L * I F R * * V L P -
b N C V D I A K E S N S K S F V N K Y Y Q -
c I A S I L Q K N R T L N L S L I S I T N -

ATCTTGATTGATTGAAGAGATTGACGAGGCAACTGCACAGAAGATCATTAAAGAAATAAA
1441 -----+-----+-----+-----+-----+-----+ 1500
TAGAACTAACTAACTTCTCTAACTGCTCCGTTGACGTGTCTTCTAGTAATTTCTTTATTT

a I L I D C R D C R G N C T E D H * R N K -
b S C L I E E I D E A T A Q K I I K E I K -
c L D C L K R L T R Q L H R R S L K K * S -

GTAACTTTTATTAAATTAGAGAATAAACTAAATTACTAATATAGAGATCAGCGATCTTCAA
1501 -----+-----+-----+-----+-----+-----+ 1560
CATTGAAAATAATTAATCTCTTATTTGATTTAATGATTATATCTCTAGTCGCTAGAAGTT

a V T F I N * R I N * I T N I E I S D L Q -
b * L L L I R E * T K L L I * R S A I F N -
c N F Y * L E N K L N Y * Y R D Q R S S I -

TTGACGAAATAAAAGCTGAACTAAAGTTAGACAATAAAAAATACAAACCTTGGTCAAAAT
1561 -----+-----+-----+-----+-----+-----+ 1620
AACTGCTTTATTTTCGACTTGATTTCAATCTGTTATTTTTTATGTTTGAACCAGTTTAA

a L T K * K L N * S * T I K N T N L G Q N -
b C R N K S C T K V R Q * K I Q T L V K I -
c D E I K A E L K L D N K K Y K P W S K Y -

ATTGAGGAAGGAAAAGAAGACCAGTTAGCAAAAGAAAAAATAAGGCAATAAAATAAAATGA
1621 -----+-----+-----+-----+-----+-----+ 1680
TAACTCCTTCCTTTTCTTCTGGTCAATCGTTTTCTTTTTTATTCCGTTATTTATTTTACT

a I E E G K E D Q L A K E K I R Q * I K C -
b L R K E K K T S * Q K K K * G N K * N E -
c C G R K R R P V S K R K N K A I N K M S -

GTACAGAAGTGAAGAAATAAAAGATTTATTTTTTTCAATAATTTATTGAAAAGAGGGGTT
1681 -----+-----+-----+-----+-----+-----+ 1740
CATGTCTTCACTTCTTTATTTTCTAAATAAAAAAAGTTATTAAATAACTTTTCTCCCCAA

a V Q K C R N K R F I F F N N L L K R G V -
b Y R S E E I K D L F F S I I Y C K E G F -
c T E V K K * K I Y F F Q * F I E K R G F -

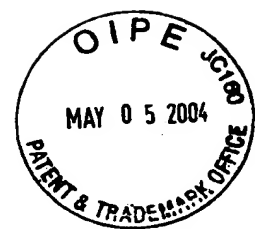
TTGGGGTTTTGGGGTTTTGGGG
1741 -----+-----+-----+-----+-----+ 1762
AACCCCAAAACCCCAAAACCCC

a L G F W G F G -
b W G F G V L G -
c G V L G F W -

FIG. 35D

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47/103



798 EKLINVSRENGFKFNMKK.LQTSFPLSPSKFAKYGMDSVEEQNIVQDYCD 846
 577PGDELRPSMQKLLQEKGLGGG..TDFPYECIDEWTKNKTHTVD 617
 847 WIGISIDMKTLALMPNINLRIEGILCTLNLNMQTKKASMWLKKKLKSFLM 896
 618 NIVILSDMMIAEGYS DINVRGSSIVNSI.....KKYKDEVN 653
 897 NNITHYFRKTITTDFANKTLNKLFISSGGYKMQCAKEYKD.HFKKNLAM 945
 654 PNIKIF...AVDLEGYG.....KCLNLGDEFNENNYIKIFGM 687
 946 SSMIDLEVSKIIYSVTRAFFKYLVCNIKDTIFGEEHYPDFFLSTLKHFI 995
 688 SDSI.....LKFISAKQGA.....NMVE 706
 996 IFSTKKYIFNRVC 1008
 707 VI..KNFALQKIG 717

FIG. 36B

132 LSTQKQYFFQDEWNQVRAMIGNEL.FRHLTYKYLIFQRTSE..GTLVQFC 178
 1 MSRRNQ.....KKPQAPIGNETNLDFVLQNLLEVYKSQIEHYKTQQQQI 43
 179 GNNVFDHLKVNDKFDKKQKGAADMNEPRCCSTCKYNVKNEKDHLNNIN 228
 44 KEEDLKLKFKNQDQDGNNGDDDEE.....NNSNKQQLLRRVN 84
 229 VPNNWNNMKSRTIRIFYCTHFNRRNQFFKKHEFVSNKNNISAMDRAQTIFTN 278
 85QIKQQVQLIKK...VGSKEKDLNLNEDENKKN 114
 279 IFRFNIRKKLKDVKIEKIAYMLEKVKDFNFNYLTKSCPLPENWRERKQ 328
 115 GLSEQQVKEEQLRTITEEQVKYQNLVFNMDYQLDLNESGGHRRHRRET DY 164
 329 KIENLINKTREEKSKYEEELFSYTTDNKCVTQFINE.FFYNILPKDFLTG 377
 165 DTEKWFEISHDQK.....NYVSIYANQKTSYCWWLKDYFNK 200
 378 RNRKNFQKKVKKYVELNKHელიHKNLLEKINTREISWMQVETSAKHFFY 427
 201 NNYDHLNVSINRLE..TEAEFYAFDDFSQTIKLTNNSYQTVNID..... 242
 428 FDHENIYVLWKLLRWI..FEDLVVSLIRCFYVTEQQKSYSKTYYYRKN 475
 243 VNFNNLCILALLRFLLSLERFNILNIRSSY..TRNQYNFEKIGELLETI 290
 476 WDVIMKMSIADLKKETLAEVQEKEVEEWKSLGFAPGKLRLIPKTTFRP 525
 291 FAVVFSHR.....HLQGIHLQVPCEAFQYLVNSSSQISVKDSQLQ 330
 526 IMTFNKKIVNSDRKT'TKLTNTKLLNSHMLKTLKNRMFKDPFGFAVFNY 575
 331 VYSFSTDLKLVD..TNKVQDYFKFLQEFPRLTHVSQQAIPVSATNAVENL 378

FIG. 37A

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48/103

576 DDVMKKYEEFVCKWKQVGQPKLF.FATMDIEKCYDS..VNREK 615
: : : | | | : : | | | : : : | | | : : : |
379 NVLLKKVKH ANLNLVSIPTQFNFDYFVNLOHLKLEFGLEPNILTKQK 426
516 LSTFL.KTTKLSSDFWIMTAQILKRKNNI..VIDSKNFRKKEMK 657
| : : | | : : | | : : | | : : | | : : |
427 LENLLLSIKQSKNLKFLRLNFYTYVAQETSRKQILKQATTIKNLKNNKNO 476
558 DYFRQKFQKIALEGGQYPTLFSVLEN..EQNDLNAKKT LIVEAKQRNYFK 705
: : : | | : : | | : : | | : : | | : : |
477 EETPETKDETPSESTSGMKFFDHLSELTELEDFSVN...LQATQEIY.. 520
706 KDNLLQPVINICQYNYINFNGKFYKQTKGIPQGLCVSSILSSFYATLEE 755
| : : | | : : | | : : | | : : | | : : |
521 .DSLHKLLIRSTNLKKFKLSYKYEMEKSKMDTFIDLKNI....YETLNN 564
756 SSLGFLRDESMNPENPNVNLMLRLTDDYLLITTQENNAVL FIEKLINVS 305
: : : | | : : | | : : | | : : | | : : |
565LKRCSVNISNPHGNISYELTN.....KDSTFYKFKLTNLQE 500

806 ENGFKFNMKKLQTSFPLSPSKFAKYGMDSVEEQNIVQDYCDWIGISIDMK 855
| : : | | : : | | : : | | : : | | : : |
601 LQHAKYTFK..QNEFQFN NVKSAKIESSSLESLEDIDSLCKSIASCKNLQ 648
856 TLALMPNINLRIEGILCTLNLMQT..KKASMWLK..KLKSFLMNNITH 901
: : : | | : : | | : : | | : : | | : : |
649 NVNI.....IASLLYPNNIQKNPFNKP NLLFFKQFEQLKNLENVSINC 691
902 YFRKTI...TTEDFANKTLNKLFISSGGYKYMQCAKEYKDHFKNLAMSSM 948
: : : | | : : | | : : | | : : | | : : |
692 ILDQHILNSISEFLEKNKKIKAFILKRYLLQYYLDYTKLFKTLQQLPEL 741
949 IDLEVSKIIYSVT.....RAFFKYLVCNIKDT..IFGEEHY 982
: : : | | : : | | : : | | : : | | : : |
742 NQVYINQOLEELTVSEVHKQVWENHKQKAFYEPLCEFIKESQTLQLIDF 791
983 PDFFLS TLKHFIEIFSTKKY IFNRVCMILKAKEAKLSDQCQSLIQ 1028
: : : | | : : | | : : | | : : | | : : |
792 DQNTVSDDSIKKILESISESKYHHYLRNLNPSQSSSLIKSENEEIQELLK 840

FIG. 37B

4 DIDLDDIENLLPNTFNKYSSSCSDKKGCKTLKSGSKSPSLTIPK..... 47
: : : | | : : | | : : | | : : | | : : |
617 NVKSAKIESSSLESLEDIDSLCKSIASCKNLQNVNIIASLLYPNNIQKNP 666
48LQKQLEFYFSDANLYNDSFLRKLVLKSQEQRVE....IETLLM 86
: : : | | : : | | : : | | : : | | : : |
667 FNKP NLLFFKQFEQLKNLENVSINCILDQHILNSISEFLEKNKKIKAFIL 716

FIG. 38



49/103

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1 MEMDIDLDDIENL.....LPNTFNKYSSSSCDKKGCKTLKSGSKSPS... 42
  | : | . . . . . | | . . . . . | : | . . . . . | | . . . . .
491 IELAIAKIIVNKNLDEIKGHTAIFSDVSGSMSTSMSSGAKKYGSVRTCLEC 540

43 .LTIPKLQKQ.....LEFYFSDANLYNDSFLRKLVLKSQEQRVEIETLL 85
  | : | . . . . . | : : | . . . . . | : : | . . . . . | | . . . . .
541 ALVLGLMVKQRCEKSSFYIFSSPSSQCNCYL.EVDLPGDELPRPSMQKLL 589

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FIG. 39

telomerase p43	LQKLEFYFSDANLYNDSFLRKLVLKSQEQRVEIETLLM
human La	ICHQUEYYFYGDFNLPRDKFLKEQI.KLDEGWVPLEIMIK
Xenopus LaA	ICEQIEYYFYGDFNLPRDKFLKQOI.LLDDGWVPLETMIK
Drosophila La	ILROVEYYFYGDFNLPRDKFLREQIGKNEDGWVPLSVLVT
S. c. Lhp1p	CLKQVEFYFSEFNFPYDRFLRTAEK.NDGWVPISTIAT

FIG. 41

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1 aactcattta attactaatt taatcaacaa gattgataaa aagcagtaaa taaaacccaa
61 tagatttaatt ttagaaagta tcaattgaaa aatggaaatt gaaaacaact aagcacaata
121 gccaaaagcc gaaaaattgt ggtgggaact tgaattagag atgcaagaaa accaaaatga
181 tatataagtt aggggttaaga ttgacgatcc taagcaatat ctcgtgaacg tcaactgcagc
241 atgtttgttg taggaaggta gttactacta agataaagat gaaagaagat atatcatcac
301 taaagcactt cttgaggttg ctgagctga tcttgagttc atctgctagt tggcagtcct
361 catccgtaat gaactttaca tcagaactac cactaactac attgtagcat tttgtgttgt
421 ccacaagaat actcaaccat tcacgaaaa gtacttcaac aaagcagtac ttttgccctaa
481 tgacttactg gaagtctgtg aatttgcata ggttctctat atttttgatg caactgaatt
541 caaaaatttg tatcttgata ggatactttc ataagatatt cgtaaggaac tcactttccg
601 taagtgttta caaagatgcg tcagaagcaa gttttctgaa ttcaacgaat actaacttgg
661 taagtattgc actgaatcct aacgtaagaa aacaatgttc cgttacctct cagttaccaa
721 caagtaaaag tgggattaaa ctaagaagaa gagaaaagag aatctcttaa ccaaacttta
781 ggcaataaag gaactctgaag ataagtccaa gagagaaact ggagacataa tgaacgttga
841 agatgcaatc aaggctttta aaccagcagt tatgaagaaa atagccaagt gatgaatgc
901 catgaagaaa cacatgaagg cacctaaaat tcttaactct accttggaaat caaagtaact
961 gaccttcaag gatctcatta agttctgcca tatttctgag cctaaagaaa gagtctataa
1021 gatccttggg aaaaaatacc ctaagaccga agaggaatac aaagcagcct ttggtgattc
1081 tgcatctgca ccttcaatc ctgaattggc tggaaagcgt aatgaagattg aaactcttaa
1141 aacatgggaa aatgaactca gtgcaaaagg caacactgct gaggtttggg ataatttaatt
1201 ttcaagcaat taactcccat atatggccat gttacgtaac ttgtctaaac tcttaaaagc
1261 cgggtgtttc gatactacac actctattgt gatcaacaag atttgtgagc ccaaggccgt
1321 tgagaactcc aagatgttcc ctcttcaatt ctttagtgcc attgaagctg ttaatgaagc
1381 agttactaag ggattcaagg ccaagaagag agaaaatatg aatcttaaag gtcaaatcga
1441 agcagtaaaag gaagttgttg aaaaaaccga tgaagagaag aaagatatgg agttggagta
1501 aaccgaagaa ggagaatttg ttaaagtcaa cgaaggaatt ggcaagcaat acattaactc
1561 cattgaactt gcaatcaaga tagcagttta caagaattta gatgaaatca aaggacacac
1621 tgcaatcttc tctgatgttt ctggttctat gactacctca atgtcaggtg gagccaagaa
1681 gtatgggttcc gttcgtactt gtctcgagtg tgcattagtc cttggtttga tggtaaaata
1741 acgttgtgaa aagtcctcat tctacatctt cagttcacct agttctcaat gcaataagtg
1801 ttacttagaa gttgatctcc ctggagacga actccgtcct tctatgtaaa aacttttgca
1861 agagaaagga aaacttggtg gtggtactga tttcccttat gagtgcattg atgaatggac
1921 aaagaataaaa actcacgtag acaatatcgt tattttgtct gatatgatga ttgcagaagg
1981 atattcagat atcaatgtta gaggcagttc cattgttaac agcatcaaaa agtacaagga
2041 tgaagtaaat cctaaccatta aaatctttgc agttgactta gaaggttacg gaaagtgcct
2101 taatctaggt gatgagttca atgaaaacaa ctacatcaag atattcggtg tgagcgattc
2161 aatcttaaag ttcatttcag ccaagcaagg aggagcaaat atggtcgaag ttatcaaaaa
2221 ctttgccctt caaaaaatag gacaaaagtg agtttcttga gattcttcta taacaaaaat
2281 ctcaccocac tttttgtttt tattgcatag ccattatgaa atttaaatat ttatctattt
2341 atttaagtta cttacatagt ttatgtatcg cagtctatta gcctattcaa atgattctgc
2401 aaagaacaaa aaagattaaa a

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FIG. 42



Motif A		Motif B	
Consensus	h--hDh---h--h	Consensus	h----+QG---SP
telomerase p123	GQPKLFFATWDIEKCYDSVNRKLSFLTKTKLL-100-KFYKQTKGIPQGLCVSSILSSFYATLEESSLGFL	telomerase p123	h-hLgh-h
Dong (LINE)	KNRNLHCTYDDYKKAFTSIHSHWLIQVLEIYKIN- 28-RQIAIKKGIYQGDLSPLWFCIALNPLSHQLHNR	Dong (LINE)	h-hLgh-h
a1 S.c. (groupII)	FGGSNWFREVDLKKCFDTISHDLIIKELKRYISD- 26-HVPVGPVVCVQAPTSALCNVALLRDLRRLAGLA	a1 S.c. (groupII)	h-hLgh-h
HIV-RT	LKKKSVTVLVDVGDAYFSVPLDEDFRKYTAFTIP- 7-GIRYQYNVLPQGWKGSPIAFQSSMTKILEPFRKQN	HIV-RT	h-hLgh-h
L8543.12	VLPELYFMKFDVKSCYDSIPRMECMRILKDALKN- 68-KCYIREDEGLFQGSLSAPIVDLVYDDLLLEFYSEFK	L8543.12	h-hLgh-h
Motif C		Motif D	
Consensus	h--YhDDhhh	Consensus	Gh-h---K
telomerase p123	-14-LMRLTDDYLLITTOENN-0-AVLFIKLIINVSRENGFKFMKKLQT-23-QDYCDWIGISI	telomerase p123	h-hLgh-h
Dong (LINE)	-16-HLIYMDIKLYAKNDKE-0-MKKLIDTTTIFSDISMQFGLDKCKT-25-KCLYKYLGFQQ	Dong (LINE)	h-hLgh-h
a1 S.c. (groupII)	-55-YVRVADDILIGVLGSKN-2-KIIKRDINNFLNS.LGLTINEEKTLLI- 4-ETPARFLGYNI	a1 S.c. (groupII)	h-hLgh-h
HIV-RT	- 4-IYQVMDDLVVGSHLEIG-1-HRTKIEELRQHLLRWGLTTPDKKHQK- 0-EPFFLWMGYEL	HIV-RT	h-hLgh-h
L8543.12	- 8-ILKLADDFLIISTDQQQ.....VINIKKLAMGGFQKYNKANR-41-IRSKSSKGIFR	L8543.12	h-hLgh-h

FIG. 40



51/103

MEIENNQAQQPKAEKLWWELELEMQENQNDIQVRVKIDDPKQYL
VNVTAACLLQEGSYQDKDERRYIITKALLEVAESDPEFICQLA
VYIRNELYIRTTTNYIVAFVHVHKNTPFIEKYFNKAVLLPNDL
LEVCEFAQVLYIFDATEFKNLYLDRILSQDIRKELTFRKCLQRC
VRSKFSEFNEYQLGKYCTESQRKKTMTFRYLSVTNKQKWDQTKKK
RKENLLTKLQAIKESDKSKRETGDIMNVEDAIKALKPAVMKKI
AKRQONAMKKHMKAPKIPNSTLESKYLTFFKDLIKFCHISEPKERV
YKILGKKYPKTEEEYKAAFSDSASAPFNPPELAGKRMKIEISKTW
ENELSAKGNTAEVWDNLISSNQLPYMAMLRNLSNILKAGVSDTT
HSIVINKICEPKAVENSKMFPLQFFSAIEAVNEAVTKGFKAKKR
ENMNLKGQIEAVKEVVEKTDEEKKDMELEQTEEGEFVKVNEGIG
KQYINSIELAIKIAVNKNLDEIKGHTAIFSDVSGSMSTSMSSGA
KKYGSVRTCLECALVLGLMVKQRCESKFYIFSSPSSQCNKCYL
EVDLPGDELPRSMQKLLQEKGLGGGTDFPYECIDEWTKNKTTHV
DNIVILSDMMIAEGYSDINVRGSSIVNSIKKYKDEVNPNIKIFA
VDLEGYGKCLNLGDEFNENNYIKIFGMSDSILKFISAKQGGANM
VEVIKNFALQKIGQK

FIG. 43

MSRRNQKKPQAPIGNETNLDVFLQNLEVYKSQIEHYKTQQQKIK
EEDLKLKFKNQDQDGNNGNDDDEENNSNKQELLRRVNQIKQ
QVQLIKKVGSKVEKDLNLNEDENKKNGLSEQQVKEEQLRTITEE
QVKYQNLVFNMDYQLDLNESGGHRRHRRETDDYDEKWFESHQDQ
KNYVSIYANQKTSYCWWLKDYFNKNNDHNLVNSINRLETEAEFY
AFDDFSQTIKLTNNSYQTVNIDVNFNNLCILALLRFLLSLERF
NILNIRSSYTRNQYNFEKIGELLETFIAVVFSHRHLQGIHLQVP
CEAFQYLVNSSSQISVKDSQLQVYSFSTDLKLVDTNKVQDYFKF
LQEFPRLTHVSQQAIPVSATNAVENLNLVLLKKVKHANLNLVSI
TQFNDFYFVNQLHLKLEFGLPNILTKQKLENLLLSIKQSKNL
KFLRLNFYTYVAQETSRKQILKQATTIKNLKNNKNEETPETKD
ETPSESTSGMKFFDHLSELTELEDFSVNLQATQEIYDSLHLLI
RSTNLKKFKLSYKYEMEKSKMDTFIDLKNIYETLNNLKRCVNI
SNPHGNI SYELTNKDSTFYKFKLTNLQELQHAKYTFKQNEFQFN
NVKSAKIESSSLESLEDIDSLCKSIASCKNLQNVNI IASLLYPN
NIQKNPFPKNPOLLFFKQFEQLKNLENVSINCLDQHILNSISEF
LEKNKKIKAFILKRYLLQYYLDYTKLFTLQQLPELNQVYINQ
QLEELTVSEVHKQVWENHKQKAFYEPLCEFIKESSTLQDLIDFD
QNTVSDDSIKKILESISESKYHHYLRNPSQSSSLIKSENEEIQ
ELLKACDEKGVLVKAYYKFPLCLPTGTYYDYNSDRW

FIG. 45

MKILFEFIQDKLDIDLQTNSTYKENLCKGHFNGLDEILTTCPAL
PNSRKIALPCLPGDLSHKAVIDHCIIYLLTGELYNNVLTFGYKI
ARNEDVNNSLFCHSANVNTLLKGAWKMFHSLVGTYA FVDLLI
NYTVIQFNGQFFTQIVGNRCNEPHLPPKWVQRSSSSSATAAQIK
QLTEPVTNKQFLHKLINSSSFFPYSKILPSSSSSIKKLTDLREA
IFPTNLVKIPQRLKVRINLTQKLLKRHKRLNVVSI LNSICPPL
EGTVLDLSHLSRQSPKERVLFIIIVILQKLLPQEMFGSKKNKGK
IIKNLNLNLLSLPLNGYLPFDSSLKLRKDFRWLFISDIWFTKH
NFENLNQLAICFISWLFRLPKIIQTFFYCTEISSTVTIVYFR
HDTWNKLITPFIVEYFKTYLVENNVCRNHNSYTLNPNHNSKMRI
IPKKSNNEFRIIAIPCRGADEEEFTYKENHKNAIQPTQKILEY
LRNKRPTSFTKIYSPTQIADRIKEFKQRLKFKFNNVLPPELYFMK
FDVKSCYDSIPRMECMRILKDALKNENGFFVRSQYFFNTNTGVL
KLFNVVNASRVKPYELYIDNVRTVHLSNQDVINVVEMEIFKTA
LWVEDKCYIREDGLFQGSLSAPIVDLVYDDLLEFYSEFKASPS
QDTLILKLADDFLIISTDQQQVINIKKLAMGGFQKYNANANRDK
ILAVSSQSDDDTVIQFCAMHIFVKELEVWKHSSTMNPFHRSKS
SKGIFRSLIALFNTRISYKTIDTNLSTNTVLMQIDHVVKNISE
CYKSAFKDLSINVTQNMQFHSFLQRIEMTVSGCPITKCDPLIE
YEVRFITLNGFLESLSNNTSKFKDNIILLRKEIQHLQAYIYIYI
HIVN

FIG. 46



1	tcaatactat	taattaataa	ataaaaaaaaa	gcaaaactaca	aagaaaaatgt	caaggcgtaa
61	ctaaaaaaaaag	ccataggctc	ctataggcaa	tgaaacaaat	cttgattttg	tattacaaaa
121	tctagaagtt	tacaaaagcc	agatttagca	ttataagacc	tagtagtaat	agatcaaaga
181	ggaggatctc	aagcttttaa	agttcaaaaa	ttaagattag	gatggaaact	ctggcaacga
241	tgatgatgat	gaagaaaaca	actcaaataa	ataataagaa	ttattaagga	gagtcaatta
301	gattaagtag	caagtttaat	tgataaaaaa	agttggttct	aaggtagaga	aagatttgaa
361	tttgaacgaa	gatgaaaaca	aaaagaatgg	actttctgaa	tagcaagtga	aagaagagta
421	attaagaacg	attactgaag	aataggttaa	gtattaaaat	ttagtattta	acatggacta
481	ccagtttagat	ttaaatgaga	gtggtggcca	tagaagacac	agaagagaaa	cagattatga
541	tactgaaaaa	tggtttgaaa	tatctcatga	ccaaaaaaat	tatgtatcaa	tttacgccaa
601	ctaaaagaca	tcatattggt	ggtggcttaa	agattatttt	aataaaaaaca	attatgatca
661	tcttaaatgta	agcattaaca	gactagaaac	tgaagccgaa	ttctatgcct	ttgatgattt
721	ttcacaaaaca	atcaaactta	ctaataattc	ttactagact	gttaacatag	acgttaattt
781	tgataataat	ctctgtatac	tcgcattgct	tagattttta	ttatcactag	aaagattcaa
841	tatttttgaat	ataagatctt	cttatacaag	aaattaatat	aattttgaga	aaattggtga
901	gctacttgaa	actatcttcg	cagttgtctt	ttctcatcgc	cacttacaag	gcattcattt
961	acaagttcct	tgcgaaagcgt	tctaattttt	agtttaactcc	tcacataaaa	ttagcgttaa
1021	agatagctaa	ttataggtat	actctttctc	tacagactta	aaattagttg	acactaacia
1081	agtccaagat	tatttttaagt	tcttataaga	attccctcgt	ttgactcatg	taagctagta
1141	ggctatccca	gttagtgcta	ctaacgctgt	agagaacctc	aatgttttac	ttaaaaaggt
1201	caagcatgct	aatcttaatt	tagtttctat	ccctaccta	ttcaattttg	atttctactt
1261	tgtaatttta	taacatttga	aattagagtt	tggtattaga	ccaaatattt	tgacaaaaaca
1321	aaagcttgaa	aatctacttt	tgagtataaa	ataatcaaaa	aatcttaaat	ttttaagatt
1381	aaactttttac	acctacgttg	cttaagaaac	ctccagaaaa	cagatattaa	aacaagctac
1441	aacaatcaaaa	aatctcaaaa	acaataaaaa	tcaagaagaa	actcctgaaa	ctaaagattga
1501	aactccaagc	gaaagcacia	gtggtatgaa	attttttgat	catctttctg	aattaaccga
1561	gcttgaagat	ttcagcgtta	acttgtaagc	tacccaagaa	atttatgata	gcttgcacaa
1621	acttttgatt	agatcaacaa	atttaaaaga	gttcaaatta	agttacaaat	atgaaatgga
1681	aaagagtaaa	atggatacat	tcatagatct	taagaatatt	tatgaaacct	ttaacaatct
1741	taaaagatgc	tctgttaata	tatcaaatcc	tcatggaaac	atttcttatg	aactgacaaa
1801	taaagattct	actttttata	aattttaagct	gaccttaaac	taagaattat	aacacgctaa
1861	gtatactttt	aagtagaacg	aattttaatt	taataacggt	aaaagtgcac	aaattgaatc
1921	ttcctcatta	gaaagcttag	aagatattga	tagtctttgc	aaatctattg	cttcttgtaa
1981	aaattttacaa	aatgttaata	ttatcgccag	tttgctctat	cccaacaata	tttagaaaaa
2041	tccttttcaat	aagcccaatc	ttctattttt	caagcaattt	gaataattga	aaaatttgga
2101	aaatgtatct	atcaactgta	ttcttgatca	gcatatactt	aattctattt	cagaattctt
2161	agaaaagaat	aaaaaaaata	aagcattcat	tttgaaaaga	tattatttat	tacaatatta
2221	tcttgattat	actaaattat	ttaaaacact	tcaatagtta	cctgaattaa	attaagttaa
2281	cattaattag	caattagaag	aattgactgt	gagtgaagta	cataagtaag	tatgggaaaa
2341	ccacaagcaa	aaagctttct	atgaaccatt	atgtgagttt	atcaaagaat	catcctaacc
2401	ccttttagcta	atagattttg	acaaaaacac	tgtaagtgat	gactctatta	aaaagatttt
2461	agaatctata	tctgagtcta	agtatcatca	ttatttgaga	ttgaacctta	gttaatctag
2521	cagtttaatt	aaatctgaaa	acgaagaaat	ttagaacttt	ctcaaagctt	gcgacgaaaa
2581	aggtgtttta	gtaaaagcat	actataaaat	ccctctatgt	ttaccaactg	gtacttatta
2641	cgattacaat	tcagatagat	ggtgattaat	taaaatttag	tttaaatata	tattaaatat
2701	tgaatatttc	tttgcttatt	atttgaataa	tacatacaat	agtcattttt	agtgttttga
2761	atatatttta	gttatttaat	tcattatttt	aagtaaataa	ttattttttc	atcatttttt
2821	aaaaaatcg					

FIG. 44



Oxytricha
Euplotes

LCVSYILSSFYYANLEENALQFLRKESMDPEKPETNLLMRLT
LCVSSILSSFYYATLEESSLGFLRDESMNPENPNVNLMLRLT

FIG. 47

ATTTATACTCATGAAAATCTTATTCGAGTTCATTCAAGACAAGCTTGACATTGATCTACA
GACCAACAGTACTTACAAAGAAAAATTTAAAATGTGGTCACTTCAATGGCCTCGATGAAAT
TCTAACTACGTGTTTCGCACTACCAAATTCAGAAAAATAGCATTACCATGCCTTCCTGG
TGACTTAAGCCACAAAGCAGTCATTGATCACTGCATCATTTACCTGTTGACGGGCGAATT
ATACAACAACGTACTAACATTTGGCTATAAAATAGCTAGAAATGAAGATGTCAACAATAG
TCTTTTTTGGCCATTCTGCAAATGTTAACGTTACGTTACTGAAAGGCGCTGCTTGGAAAAAT
GTTCCACAGTTTGGTCGGTACATACGCATTCTGTTGATTTATTGATCAATTATACAGTAAT
TCAATTTTAATGGGCAGTTTTTCACTCAAATCGTGGGTAAACAGATGTAACGAACCTCATCT
GCCGCCCAAATGGGTCCAACGATCATCCTCATCATCCGCAACTGCTGCGCAAATCAAACA
ACTTACAGAACCAAGTGACAAATAACAATTTCTTACACAAGCTCAATATAAATTCCTCTTC
TTTTTTTCTTATAGCAAGATCCTTCCTTCATCATCTATCAAAAAGCTAACTGACTT
GAGAGAAGCTATTTTCCCAAAAATTTGGTTAAAATTCCTCAGAGACTAAAGGTACGAAT
TAATTTGACGCTGCAAAAGCTATTAAAGAGACATAAGCGTTTGAATTACGTTTCTATTTT
GAATAGTATTTGCCACCATTGGGAAGGGACCGTATTGGACTTGTGCGCATTTGAGTAGGCA
ATCACCAAAGGAACGAGTCTTGAAATTTATCATTGTTATTTTACAGAAAGTTATTACCCCA
AGAAATGTTTGGCTCAAAGAAAAATAAGGAAAAATTTATCAAGAATCTAAATCTTTTATT
AAGTTTACCCTTAAATGGCTATTTACCATTTGATAGTTTGTGAAAAAGTTAAGATTAAA
GGATTTTCGGTGGTTGTTTCTGATATTTGGTTTACCAAGCACAATTTTGAAAACCTT
GAATCAATTGGCGATTTGTTTCTTCTGGCTATTTAGACAACTAATTCCTAAAATTTAT
ACAGACTTTTTTTTACTGCACCGAAATATCTTCTACAGTGACAATTGTTTACTTTAGACA
TGATACTTGGAATAAACTTATCACCCCTTTTATCGTAGAATATTTTAAAGACGTACTTAGT
CGAAAACAACGTATGTAGAAACCATAATAGTTACACGTTGTCCAATTTCAATCATAGCAA
AATGAGGATTATACCAAAAAAAGTAATAATGAGTTCAGGATTATTGCCATCCCATGCAG
AGGGGCAGACGAAGAAGATTCACAATTTATAAGGAGAATCACAAAATGCTATCCAGCC
CACTCAAAAATTTTAGAATAACCTAAGAAACAAAAGGCCGACTAGTTTACTAAAATATA
TTCTCCAACGCAAAATAGCTGACCGTATCAAGAATTTAAGCAGAGACTTTTAAAGAAAT
TAATAATGTCTTACCAGAGCTTTATTTTCATGAAATTTGATGTCAAATCTTGCTATGATTC
CATACCAAGGATGGAATGTATGAGGATACTCAAGGATGCGCTAAAAAATGAAAATGGGTT
TTTCGTTAGATCTCAATATTTCTTCAATACCAATACAGGTGTATTGAAGTTATTTAATGT
TGTTAACGCTAGCAGAGTACCAAAACCTTATGAGCTATACATAGATAATGTGAGGACGGT
TCATTTATCAAATCAGGATGTTATAACGTTGTAGAGATGGAATATTTAAAACAGCTTT
GTGGGTTGAAGATAAGTGCTACATTAGAGAAGATGGTCTTTTTTCAGGGCTCTAGTTTATC
TGCTCCGATCGTTGATTTGGTGTATGACGATCTTCTGGAGTTTATAGCGAGTTTAAAGC
CAGTCCTAGCCAGGACACATTAATTTTAAAACCTGGCTGACGATTTCTTATAATATCAAC
AGACCAACAGCAAGTGATCAATATCAAAAAGCTTGCCATGGGCGGATTTCAAAAATATAA
TGCGAAAGCCAATAGAGACAAAATTTTAGCCGTAAGCTCCCAATCAGATGATGATACGGT
TATTCATTTTGTGCAATGCACATATTTGTTAAAGAATTGGAAGTTTGGAACATTCAAG
CACAATGAATAATTTCCATATCCGTTTCAAAATCTAGTAAAGGGATATTTTCAAGTTTAAT
AGCGCTGTTTAACTAGAAATCTCTTATAAAACAATTGACACAAATTTAAATTCACAAA
CACCGTTCTCATGCAAATTTGATCATGTTGTAAAGAATTTTCGGAATGTTATAAATCTGC
TTTTAAGGATCTATCAATTAATGTTACGCAAAATATGCAATTTTCAATTCGTTCTTACAACG
CATCATTGAAATGACAGTCAGCGGTTGTCCAATTACGAAATGTGATCCTTTAATCGAGTA
TGAGGTACGATTCACCATATTGAATGGATTTTGGAAAGCCTATCTTCAAACACATCAAA
ATTTAAAGATAATATCATTCTTTTGAGAAAGGAAATTCACACTTGCAAGC

FIG. 48

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54/103



AKFLHWLMSVYVVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKR
VQLRDVSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREK
RAERLTSRVKALFSVLNYERA

FIG. 49

GCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTC
TTTCTTTTATGTCACGGAGACCACGTTTCAAAGAAGCAGGCTCTTTTCTACC
GGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAG
AGGGTGCAGCTGCGGGACGTGTGCGAAGCAGAGGTCAGGCAGCATCGGGAAGC
CAGGCCCCGCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGACGGGC
TGCGGCCGATTGTGAACATGGACTACGTGCTGGGAGCCAGAACGTTCCGCAGA
GAAAAGAGGGCCGAGCGTCTCACCTCGAGGGGTGAAGGCACTGTTTCAGCGTGCT
CAACTACGAGCGGGCGCG

FIG. 50

MTEHHTPKSRILRFLNQYVYLCTLNDYVQLVLRGSPASSYSNICERLRSDVQTSFSIFLHSTVVGF
DSKPDEGVQFSSPKCSQSELIANVVKQMFDESERRRNLMLKGFSMNHEDFRAMHVNGVQNDLVSTF
PNYLISILESKNWQLLEIIGSDAMHYLLSKGSIFEALPNDNYLQISGIPLFKNNVFEETVSKKRKR
TIETSITQNK SARKEVSWNSISISRFSIFYRSSYKKFKQDLYFNLHSICDRNTVHMLQWIFPRQFG
LINAQVQQLHKVPLVSQSTVVPKRLKVPYPLIEQTAKRLHRISLSKVYNHYCPYIDTHDDEKILS
YSLKPNQVFAFLRSILVRVFPKLIWGNQRIFEIILKDLETFLKLSRYESFSLHYLMSNIKISEIEWL
VLGKRSNAKMCLSDFEKRKQIFAEFIYWLNSFIIPILQSFFYITESSDLNRNRTVYFRKDIWLLCR
PFITSMKMEAFEKINENNVRMDTQKTTLPFAVIRLLPKKNTFRLITNLKRFLIKMGSNNKMLVSTN
QTLRPVASILKHLINIESSGIPFNLEVYMKLLTFKKDLLKHRMFGRKKYFVRIDIKSCYDRIKQDLM
FRIVKKKLDPEFVIRKYATIHATSDRATKNFVSEAFSYFDMVPFEKVQLLSMKTSDTLFDVDFDY
WTKSSSEIFKMLKEHLSGHIVKIGNSQYLQKVGIPQGSILSSFLCHFYMEDLIDEYLSFTKKKGSVL
LRVDDDFLITVNKKDAKKFLNLSLRGFEKHNFTSLEKTVINFENSNGIINNTFFNESKKRMPFFG
FSVNMRLDITLLACPKIDEALFNSTVELTKHMGKSFFYKILRSSLASFAQVFIDITHNSKFNSCCN
IYRLGYSMCMRAQAYLKRMDIFIPQRMFITDLLNVIGRKIWKLAELGYTSRRFLSSAEVKWLFC
LGMRDGLKPSFKYHPCFEQLIYQFQSLTDLIKPLRPVLRQVFLHRRID

FIG. 51

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ggtaaccgattacttcttcttccataagctaattgcttctcctcgaaacgctcctaaaaatctctggaataatatttttacaaga
 actcaataaacaataccaagtaactccaaatccaaatagaggtgttattagtagcgaataatattcttatttttattcgggtgta
 ccaagtataaggacaaaaaagaacaacttcttcccccaaaagacttttactttataatttttacttttcaaatataatttcg
 ggttcgcttacttttaactggtgactgttttagtgcacttctagccaacgggtgtttctaccccgctcatggatat
 agtcttggagtagtcacagaaacttcaaaaacttctgatgagactataatagattcattacagtcggtgcataatc
 ttaacatggagccttacacttttagatgagtcagtcgcatgaggtatattggtatcatccaaggtttgccttgaaaaag
 gttgataattatttgcaaaatcactgcttagtggttaacgcgaaaagttttttagcttgcacacgctcagcatg
 attgagataattcaaaaatttctaccactacaactccttaacgggttttatttttcttatttctcactatcccccattgtt
 ccaaatatgtatcatctcgtattaggctttttccggttttactcctggaaatcgtaacctttttcactattcccccaatga
 ataactaaatagtttcgcttaataatgatagtagtaaaagattggtgattcactcgtgaatgttattagtttaaa
 gatacttgcaaaacatttattagctatcattatataaaaaaaactcctataatataaaatattcaaatatttgoggtc
 actatttatttaaaacggttatgacagtaggacactttgcataatatagttatgcttaattggttacttgaactgtcat
 GACCGAACACCATACCCCAAAGCAGGATTTTCGCTTTCTAGAGAAATCAATATGTATACCTATGTACCTTTAAATGATT
 ATGTACAACTTTGTTGAGAGGTCGCGGCAAGCTGTATAGCAATATATGCGAAAGCTTGAGAACGGATGTACAAACG
 TCCTTTTCTATTCTTCATTTCGACTGTAGTCGCTTCGACAGTAAGCCAGATGAAGGTGTTCAATTTTCTTCCTCAA
 ATGCTACAGTCAGAGgtatataattttggtttgatttttcttattcgggtagtaataatattggcgagctaaTAGC
 GAATGTTGTAACACAGATGTTTCGATGAAGTTTGTAGCGTCGAAGGAATCTACTGATGAAGGGTTTCCATGgttaaggt
 attcctaattgtgaataatttacctgcaattactgtttcaaaagagattgtatttaaccgataaagAATCATGAAGATTTC
 GAGCCATGCATGTAACGGAGTACAAAATGATCTGTTCTACTTTCTTAATTAACCTTATCTATATCTTGTAGTCAAAA
 AATTGGCAACTTTTGTAGAAATgtaaatccgggttaagatgttgcgcaacttgaacaagaatgacaagtagtatCGG
 CAGTGATGCCATGCTACTTATTATCCAAAGGAAGTATTTTTCAGGCTCTTCCAAATGACAAATACCTTCAGATTCTTG
 GCATACCACTTTTAAATAATATGTGTTGAGGAACTGTGTCAAAAAGAACCAATGAAACATCCATTAAT
 CAAAATAAAGCGCCGCAAGAAAGTTTCCTGGAATAGCATTTCAATTAGTAGTTTAGCATTTTTCACAGTCACTTA
 TAAGAAATTAAGCAAGgttaactaatactgtttactcctcatactaatatttagatcttataatttttaacttACACTTATT
 GTGATCGGAACACAGTACACATGTGGCTTCAATGGATTTTTCGAAGGCAATTTGGACTTATAAAGCAATTCAGTGAAG
 CAATGCAACAAAGTATCCACTGGTATCACAGAGTACAGTTGTGCCCAACCGTCTCTAAAGGTATACCTTTAATGA
 ACAACAGCAAGCACTCCATCGTATTCTCTATCAAAAGTTTACAACCAATATTGCCCATATATGACACCCAGATG
 ATGAAAAATCCTTAGTTATTCCTTAAAGCCGACCAAGGTGTTGCGTTTCTTCGATCCATTCCTTGTTCGAGTGTTCCT
 AAATAATCTGGGTAAACCAAGGATATTGAGATAATATTAAAGgtattgtataaaaatttaccactaaagatttt
 accagACCTCGAAACTTTCTTGAAATTAACGATACGAGTCTTTTAGTTTACATTTAATGAGTAACATAAAGgtaa
 tatgcaaaattttttaccatttaataacaatcagATTTTCAGAAATTTGAATGGCTAGTCTCTTGGAAGAAAGGTCAATGCG
 AAAATGTCTTAAGTATTTTGAGAAACGCAAGAAATATTTCGGGAATTCATCTACTGGCTAGTATCAATTCGTTTATAAT
 ACCTATTTTCAATCTTTTATATCACTGAATCAAGGTATTACGAATCGAACTGTTTATTATTAGAAAAAGATATT
 GGAAACTCTTGTGCGACCCCTTTATACATCAATGAATGGAAGCGTTTGAAAAATAAAGCAAGgtatttttaagatt
 ttttgcaaaaagcctaataatttcagAACAAATGTAGGATGGATCTCAGAAAACTACTTTTCCCTCCAGCAGTTATTCGTC
 TATTACCTAAGAGAATACCTTTCGTCTCAATTAGCAATTTAGAAAAAGATTTTAAGAGgtatttaatttttgggtcat
 caatgtacttttacttctaattattagcagATGGTTTCAACAAAAAATTTAGTCAGTACGAACCAAACTTTACG
 ACCTGTGGCATCGATACGATAACCAATTTAATCAATGAAGAAAGTAGTGGTATTCCATTTAATCTTGAGGTTTTACATGAAGC

FIG. 52A



TTCTTACTTTTAAAGAGGATCTTCTTAAGCACCAGAAATGTTTGGGtaattataaatgcgagattccctcattattaaat
 9cagCGGTAAAGAAAGTATTTGTACGGATAGATATAAAATCTGTATTGATGCAATAAAGCAAGATTTGATGTTTCGGATT
 GTTAAAGAAACTCAAGGATCCCGAATTTGTAATTCGAAGATGCAACATACATGCAACAAGTGACCGAGCTACAAA
 AAACTTTGTAGTGAGGCGTTTCCCTATTgtaagtttatttttcatggaattttttaaacaattcttttttagTTGAT
 ATGGTGCCCTTTGAAAAGTCGTGCGATTACTTTCTATGAAAACATCAGATACTTTGTTTGTGATTTTGTGATATTG
 GACCAAAAGTTCTTCTGAAATTTTAAATGCTCAAGGAACATCTCTGGACACATTTGTTAAGgtataccaattgttga
 attgataaacactaatgaaactagATAGGAAATTTCTCAATACCTTCAAAAGTTGGTATCCCTCAGGGCTCAATTTCTGT
 CATCTTTTGTGTCTATTCTATATGGAAGATTTGATTGATGAATACCTATCGTTTACGAAAAGAAAGGATCAGTGTG
 TTACGAGTAGTCAGCAATTTCTCTTTTAAACAGTTAATAAAGGATGCAAAAATTTTGAATTTATCTTTAAGAGg
 tgagttgctgtcatctcctaagttctaaccgttgaagGATTTGAGAAACACAAATTTTCTACGAGCCTGGAGAAAACAGTA
 ATAACTTTGAAAATAGTAATGGGATATAAACAATACTTTTAAATGAAGCAAGAAAAGAAATGCCATTTCTCGGTTT
 CTCTGTGAACATGAGGTCTTTGATACATGTTTAGCATCTCTAAATTTGATGAAGCCTTATTTAACTCTACATCTGTAG
 AGCTGACGAAACATATGGGAAATCTTTTACAAAATTTCTAAGgtatctgtgaactgaataaatagctgacaaata
 atcagATCGAGCCTTGATCTCTATGTTGATGAGAGCACAGCATACTTAAAGGATGAAGGATATATTTATTTCCCAAGAA
 ATATAGGCTAGGATACTCTATGTTGATGAGAGCACAGCATACTTAAAGGATGAAGGATATATTTATTTCCCAAGAA
 TGTTCAATAACGGgtgagttacttattttaactagaaaagtcatttaattaaccttagATCTTTTGAATGTTATTGGAAGAA
 AATTTGGAAGAAAGTTGCCGAAATATTAGGATATACGATAGGCGTTTCTGTCTCTGCAAGATCAAAATGgtacgtgt
 cggctcgagacttcagcaaatattgacacatcagGCTTTTGTCTTGGATGAGAGATGGTTGAAACCCCTTTTCAA
 TATCATCTGCTCGAACAGCTAATATACCAATTTCAAGTCAATGACTGATCTTATCAAGCGCTTAAGACCGATTTTGGG
 ACAGGTGTTATTTTACATAGAAATAGCTGATTAAGtcatcttcaatttattataacatcccttttactggtgtc
 ttaacaatatattactaagtatagctgaccccccaagcataactataggatttctagtaaaagtaaaataatctc
 gttattagttttagttgactgtcttattcttataactttaagaaagattgacagtggttctgactactgccccacatg
 cccattaaacgggagtggttaaacattaaaagtaatacatgaggtaactctcttcaattagaataaagaaagtgtgtt
 tctataatgaataaatgcccgcactaatgcaaaaagacgaagattatctctaaacaaggggattaaagcataatccgaag
 aaaagagagtaataataccagtggtgttgaaagaaagcaaggaataattggaacaagcttctgcagatgacaggctaaatt
 ttggtgaccgaatttttggtaaaagccccaggttatccatggtggccgcttgcactgagacgaaaaaactaaaggt
 agtttgataactaatagctcatttaagtcttataataaggttttgttttctgactcaatttgcaggggtgaaaag
 aaatgltgtaagccattattggattccgaataagccaaattcttggttcctcaaggggaagctcaagaaacttattg
 aagcttatgaggttcaaaaactcctcctgatttaaaggaggaattctccaccgatgaggaatggatagcttatcagct
 gctgaggaagagccctaatttttgcaaaaaagaaaatacatctgggagacatctcttgatgaatcagatcgaggagat
 ctccagcggtccttgatgtcaataaacttctatttctgaaatgatatggtcctactgtcgtctcacttctcgtagctta
 cgcagttaaagtaccaaaaggtacc

FIG. 52B

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EST2 pep	FFYCTEISST VTIVVFRHDT WN-----KLIT P-----FIVE YFK-TYLVEN	40
Euplotes pep	FFVYTEQOKS YSKTYYYRKN IWDVI-MKMS IAD-----LKK ETLA--EVQE	43
Trans of tetrahymen	-----KHKE GSQIFYRKP IWKLVSCLTI VKVRIQFSEK NKQMKNNFYQ	44
Consensus	FFY.TE..K..S..YYRK. IW....-KL...-F..K.....V..	50
EST2 pep	NVCRNHSY- ----- TLSNFNHSKM RIIPKKSNNNE FRITAIPCRG	79
Euplotes pep	KEVEEWKSL ----- --GFAPGKG RLIPKKT-- FRPIMTFNKK	78
Trans of tetrahymen	KIQLEENLE KVEEKLIPED SFQYPQGKL RIIPKKGSG-- FRPIMTFLRK	92
Consensus	K...E..... -----F..GKL RIIPPKK... FRPIMTF.RK	100
EST2 pep	ADEEEFTIYK ENHKNAIQPT QKILEYLRNK RPTSFTKIYS PTOIADRIKE	129
Euplotes pep	IVNSDRKTIK LTTNTKLLNS HLMKTLKN- -----RMFK -DPFGFAVEN	120
Trans of tetrahymen	DKQKNIK--- LNLNQILMDS QLVFRNLKD- -----ML-G -QKIGYSVFD	130
ConsensusK..K LN.N..L..S QL.L..LKN- -----...-IG..VF.	150
EST2 pep	EKQRLLLKFN NVL----- -PELYFMKFD VKSCYD	157
Euplotes pep	YD-DVMKKYE EFVCKWKQVH CPKLPFFATMD IEKCYD	155
Trans of tetrahymen	NK-QISEKFA QFIEKWKNGK RPCLYYVTL- -----	158
Consensus	.K-....KKF. .F...KWK..G .P.LYF.T.D ...CYD	186

FIG. 53

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58/103



S-1: FFY VTE TTF QKN RLF FYR KSV WSK
 S-2: RQH LKR VQL RDV SEA EVR QHR EA
 S-3: ART FRR EKR AER LTS RVK ALF SVL NYE

A-1: AKF LHW LMS VYV VEL LRS FFY VTE TTF Q
 A-2: LFF YRK SVW SKL QSI GIR QHL KRV QLR DVS
 A-3: PAL LTS RLR FIP KPD GLR PIV NMD YVV

FIG. 54

Poly 4

			t		t		c		
	t	a	a	g	c	c	t	c	g
5'-	cag	acc	aaa	gga	att	cca	taa	gg	-3'
	Q	T	K	G	I	P	Q	G	

4(B')

5(c')

	D	D	Y	L	L	I	T	
3'-	ctg	ctg	atg	gag	gag	tag	tgg	-5'
	a	a	a	a	a	a	a	
				t	t	t	t	
						c	c	

Poly 1

FIG. 56

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59/103

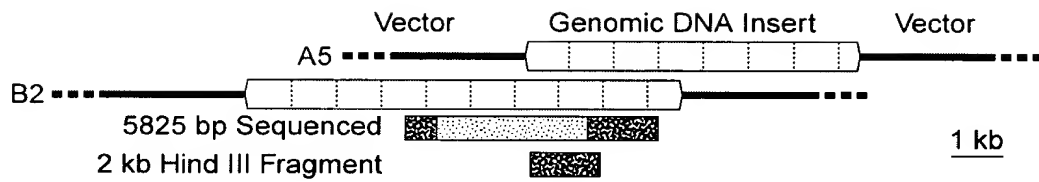


FIG. 55A

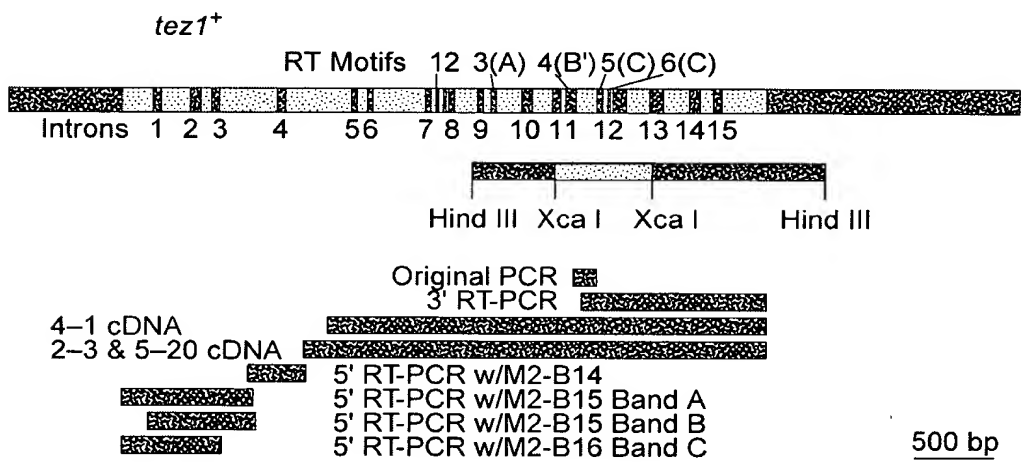


FIG. 55B

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60/103

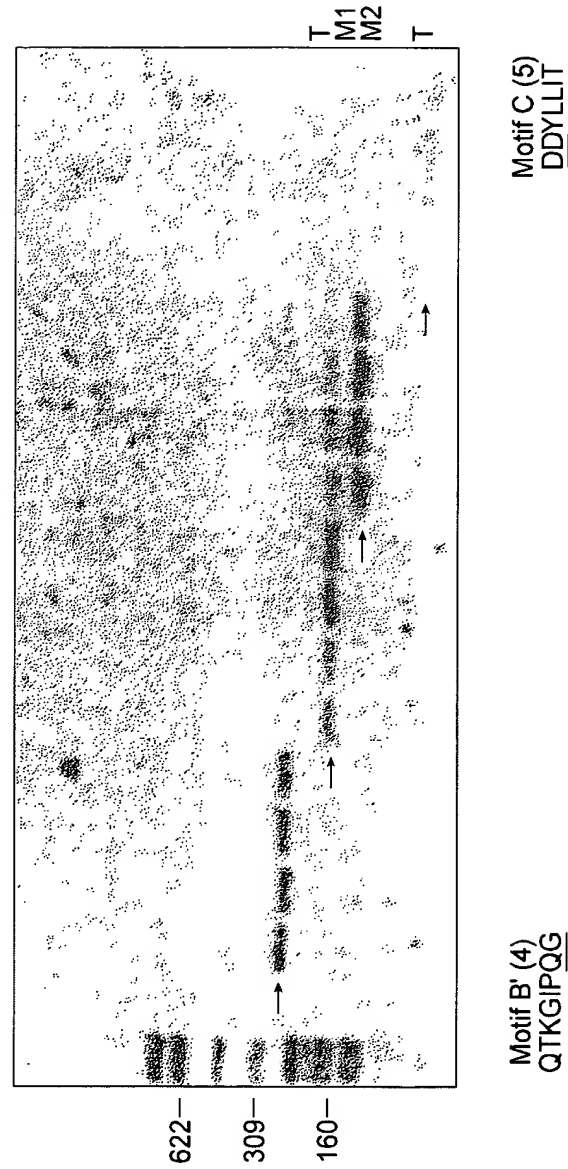


FIG. 57

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61/103

Ot LCVSYLSFFYYANLEENALQFLRKESMDPEKPETNLLMRLT
Ea_p123 KGIPQGLCVSSILSSFFYYATLEESSLGLRDESMNPENNVNLLMRLTDDYLLIT
Sp_M2 SILSSFLCHFYMEDLLIDEYLSFTKKK-----GSVLLRVV
Sc_p103 DGLFQGSLSAPIVDLVYDDLLEFYSEFKASPS-----QDTLILKLADDFLIIS
* . . *

Q K V G I P Q G
caa aaa gtt ggt atc cct cag gg..... <---Actual Genomic Sequence.

Poly 4

t t c
t a g c c t c g
cag acc aaa gga att cca taa gg ---->

ag acc aaa gga att cca tca ggc tca att ctg tca tct ttt ttg tgt cat ttc tat atg
tc tgg ttt cct taa ggt agt ccg agt taa gac agt aga aaa aac aca gta aag ata tac

K G I P S G S I L S S F L C H F Y M

FIG. 58A

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GAA GAT TTG ATT GAT GAA TAC CTA TCG TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA
CTT CTA AAC TAA CTA CTT ATG GAT AGC AAA TGC TTT TTC TTT CCT AGT CAC AAC AAT GCT
E D L I D E Y L S F T K K K G S V L L R

GTA GTC gac gac tac ctc ctc atc acc
CAT CAG ctg ctg atg gag gag tag tgg

V V D D Y L L I T

<----- ctg ctg atg gag gag tag tgg
a a a a a a a t t t
c c
Poly 1

.....gac gat ttc ctc ttt ata aca..... <---Actual Genomic Sequence
D D F L F I T

FIG. 58B

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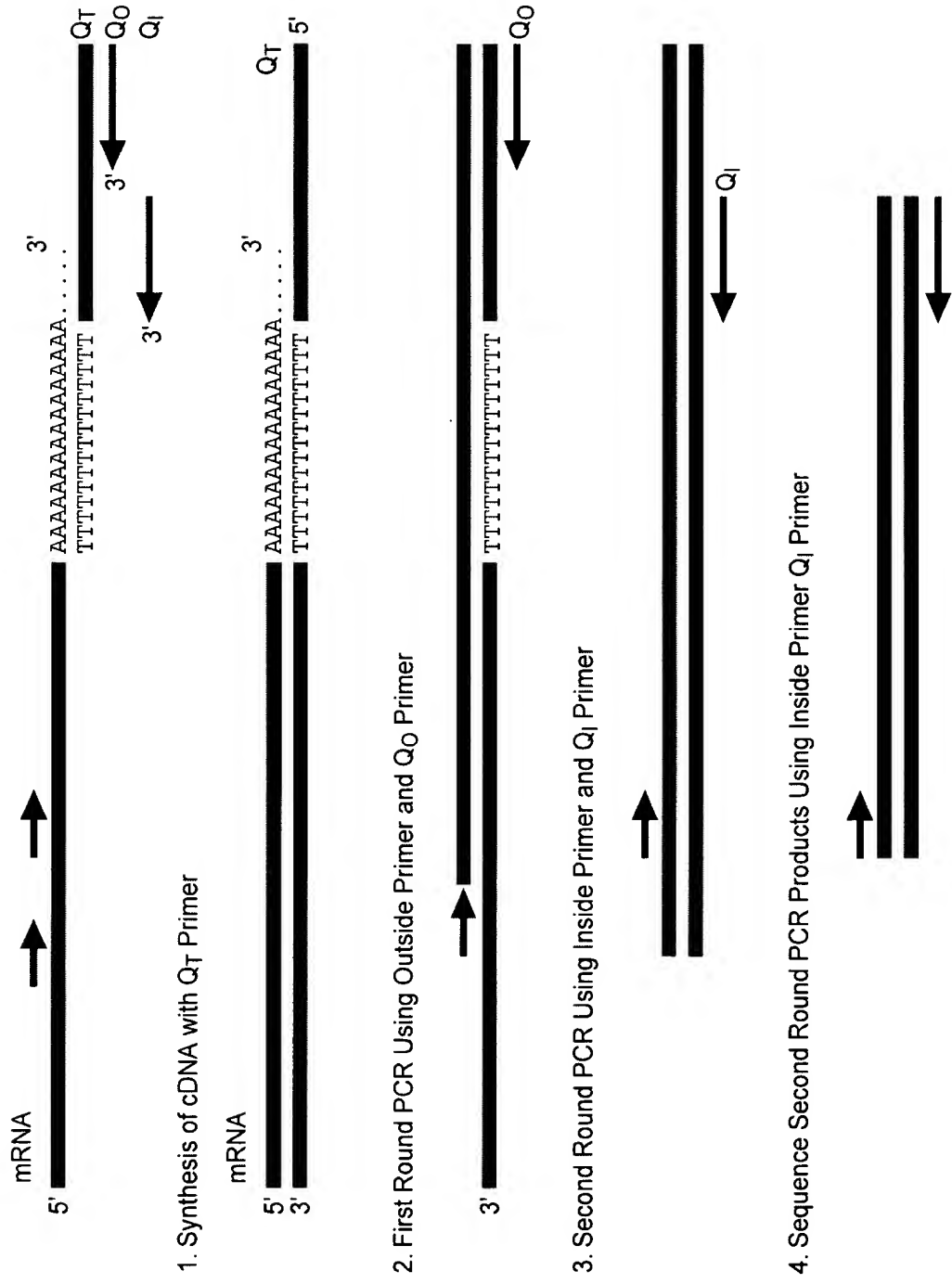


FIG. 59

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- A. Genomic Libraries**
- Size Selected Libraries from P. Nurese
 - 3~4 kb
 - 5~7 kb
 - 7~8 kb
 - 11~12 kb
 - Libraries from J.A. Wise
 - Sau 3a Partial Digest
 - Hind III Partial Digest
- cDNA Libraries**
- GAD (Gal Activation Domain) Library
 - REP Library from R. Allshire
 - REP81ES Library (old)
 - REP81ES Library (new)
 - REP41ES Library

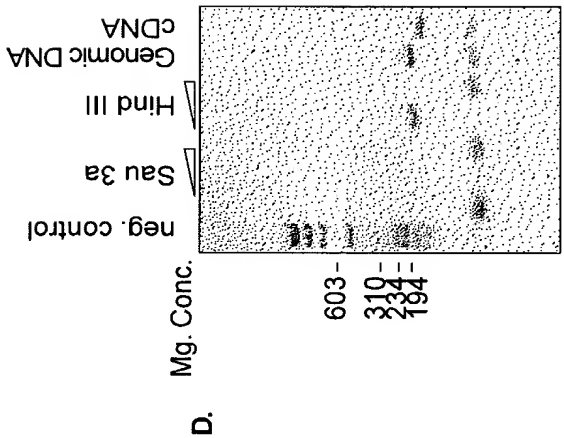
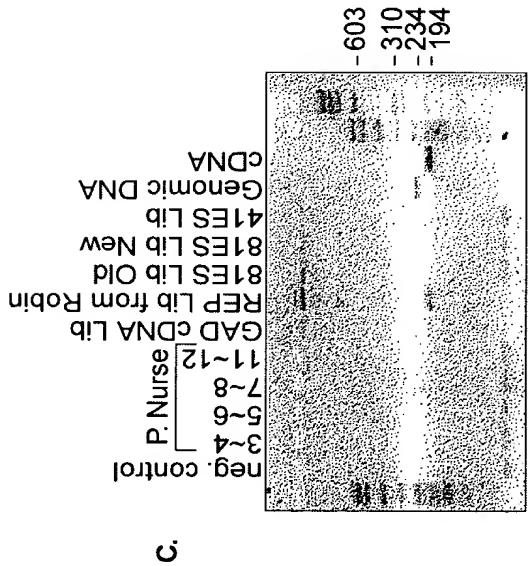
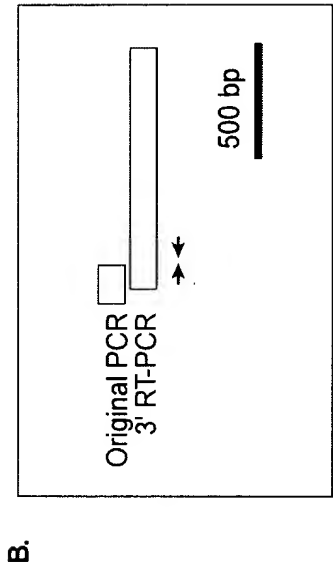


FIG. 60

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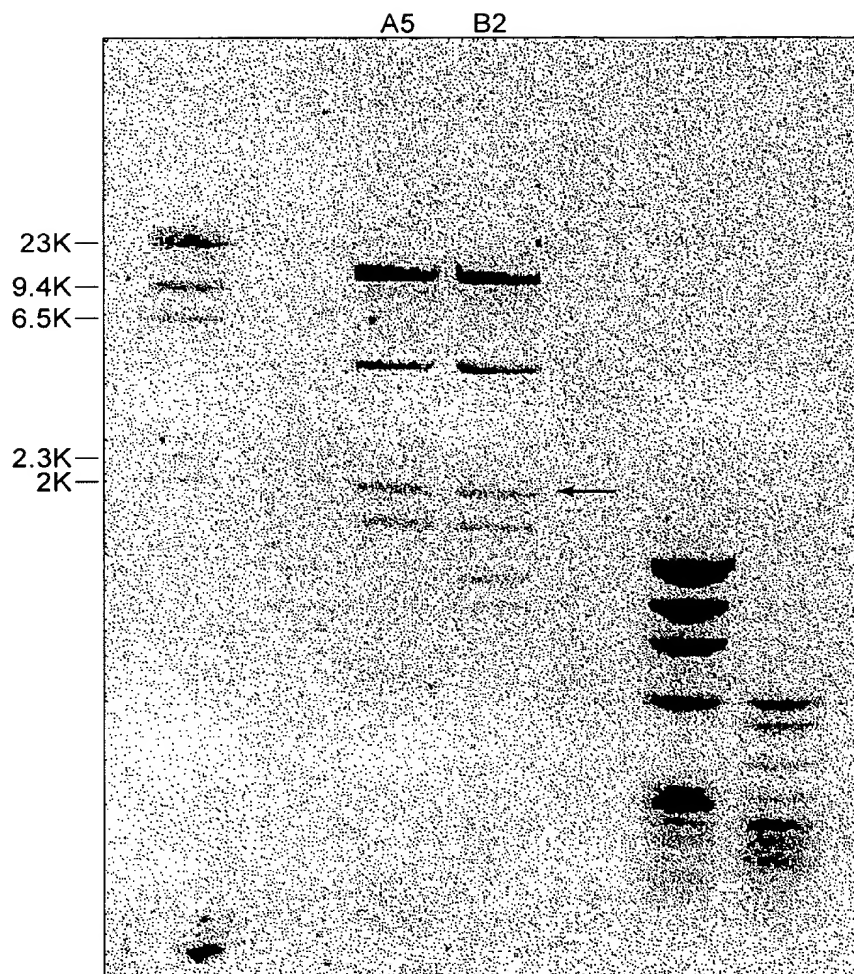
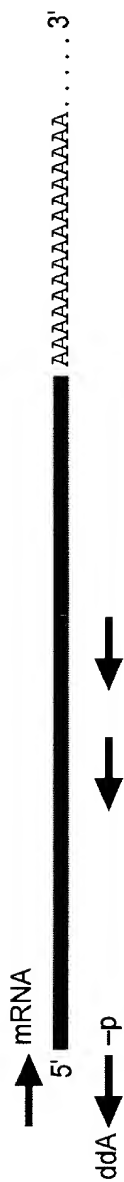
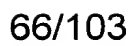
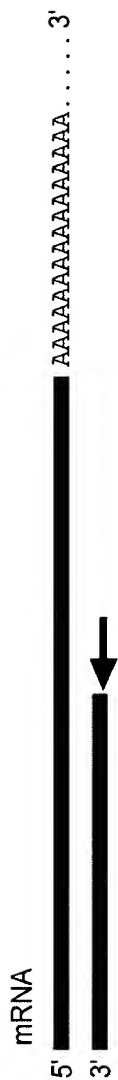


FIG. 61



1. Synthesis of cDNA with Specific Destination Primer



2. Ligate Oligo with 5' -P and blocked 3' to cDNA using T4 RNA Ligase



3. First Round PCR



4. Second Round PCR



FIG. 62



Motif O

S.p. Tez1p	(429) . WLYNSFIIPILQSFYFITESSDLRNRTVYFRKDIW	... (35) ...
S.c. Est2p	(366) . WLFRLIPKIIQTFFCYCTEISSTVT-IVYFRHDTW	... (35) ...
E.a. p123	(441) . WIFEDLVVSLIRCFVVFTEQQKSYKTYYYRKNIW	... (35) ...
	*** ** *	* * *
	Motif 1	Motif 2
	p hh h K	K
	hR h	R
S.p. Tez1p	AVIRLLPKK--NTFRLLTN-LRKRF	... (61) ...
S.c. Est2p	SKMRIIPKKSNNFEFRIAPCRGAD	... (62) ...
E.a. p123	GKRLIPKK--TTFRPIMTFNKKIV	... (61) ...
	* *** ** *	
	Motif 3 (A) AF	
	h hDh GY h	
S.p. Tez1p	KKYFVRIDIKSCYDRIKQDLMFRIVK	... (89) ...
S.c. Est2p	ELYFMKFDVKSCYDSIPRMECMRILK	... (75) ...
E.a. p123	KLFFATMDIEKCYDSVNRKLSFLK	... (107) ...
	* * * ***	*
	Motif 4 (B')	
	hpQG pp hh h	
S.p. Tez1p	YLQKVGIPQGSILSSFLCHFYMEDLLDEVLSF	... (6) ...
S.c. Est2p	YIREDGLFQGSLSAPIVDLVYDDLLLEFYSEF	... (8) ...
E.a. p123	YKQTKGIPQGLCVSSILSSFYATLEESSIGF	... (14) ...
	* * * * *	*
	Y Motif 5 (C)	Motif 6 (D)
	h F DDhhh	Gh h cK h
S.p. Tez1p	VLLRVVDDFLFITVNNKKDAKFNLISLRGFEKHNFTSLEKTVINFENS	... (205)
S.c. Est2p	LILKLADDFLIISTDQQQVINTIKLAMGGFQKYNANAKNRDKILLAVSSQS	... (173)
E.a. p123	LLMRLTDDYLLITTTQENNAVLFIKLINVSRENGFKFNMKKLQTSFPLS	... (209)
	*** ** *	* * *

FIG. 63



A.

	-	-	-	-	-	MTEHHTPKSRILRFL	ENQYVYLCT	24
Sp_Tip1p	1	-	-	-	-	-	-	
Sc_Est2p	1	-	-	-	-	-	-MKILFEF	7
Ea_p123	1	MEVD	VDNQADNHG	IHSALKTCEEI	KEAKTL	YSW		33
		LND	YVQLVL	RGS	PASS	YSNICE	RLRS	57
Sp_Tip1p	25	IQD	KLDIDL	QTN--	STYK--	ENLKCGH	FNGLD	35
Sc_Est2p	8	IQK	VIRCRNQ	SQ--	SHYK--	DLEDIKI	FAQTN	61
Ea_p123	34							
		IFL	HSTVVGFD	SKPDEGVQFSS	PKCSQS	ELIAN		90
Sp_Tip1p	58	EILT	TTCFALPN	SR-KIALPCLP	GDLSHKAVIDH			67
Sc_Est2p	36	IIVAT	PRDYNEEDFKV	IARKEVFSTGLM	IELIDK			94
Ea_p123	62							
		VVKQM	FDES	FERRR-NLL	MKGFSMN	HEDFRAMH		122
Sp_Tip1p	91	CII	YLLTGELYN--	NVLTFGYKIARNED--	--			93
Sc_Est2p	68	CLVELL	SSSDVS	DRQKLQCFFG	QLKGNQ--	--		122
Ea_p123	95							
		VNGVQN	DLVSTFPNP	NYLISIL	ESKNWQLLLEIG			155
Sp_Tip1p	123	--	VNNSLFCHS	ANVNVTLL	LKGAAWKMFHSLVG			123
Sc_Est2p	94	--	LAKTHLLT	ALSTQKQYFFQDEWN	QVRAMIG			152
Ea_p123	123							
		SDA	MHYLL	SKGSIFEAL	PNDNYLQISGIPL	EKN		188
Sp_Tip1p	156	TYAF	VDLLIN	YTVIQFN-GQFFTQ	LVGNRCNEP			155
Sc_Est2p	124	NEL	FRHL	YTKYLIFQR	TSEGTLVQFCGN	NVFDH		185
Ea_p123	153							
		NVFEET	VSKKR	KRTIETSI	TQN--	-KSARK	EVSV	218
Sp_Tip1p	189	HLP	PKWVQ-R	SSSSSA	TAAQI--	-KQLTE	EPVT	183
Sc_Est2p	156	LKV	NDKFDK-KQK	GGAADMNE	PRCCSTCKYN	VK		217
Ea_p123	186							

FIG. 64A



A.

Sp_Tip1p	219	W	N	S	I	S	I	S	R	F	S	I	F	Y	R	S	S	Y	K	K	F	K	Q	Q	D	L	Y	F	N	L	H	S	I	C	D	251		
Sc_Est2p	184	N	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	K	Q	F	L	H	K	L	N	I	N	S	S	S	F	F	P	200			
Ea_p123	218	N	E	K	-	-	D	H	F	L	N	N	I	N	V	P	N	W	N	N	M	K	S	R	T	R	I	F	Y	C	T	H	F	N	248			
Sp_Tip1p	252	R	N	T	V	H	M	W	L	Q	W	I	F	P	R	Q	F	G	L	I	N	A	F	Q	V	K	Q	L	H	K	V	I	P	L	284			
Sc_Est2p	201	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	S	I	K	K	L	T	D	L	R	E	A	I	F	P	223				
Ea_p123	249	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	N	Q	F	F	K	K	H	E	F	V	S	N	K	N	I	275			
Sp_Tip1p	285	V	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Q	S	T	V	V	P	K	R	L	L	K	V	Y	P	L	313			
Sc_Est2p	224	T	N	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	L	V	K	I	P	Q	R	L	K	V	R	I	N	L	T	252			
Ea_p123	276	F	T	N	I	F	R	F	N	R	I	R	K	K	L	K	D	K	V	I	E	K	I	A	Y	M	L	E	K	V	K	D	F	N	308			
Sp_Tip1p	314	L	S	K	V	Y	N	H	Y	C	P	Y	I	D	-	T	H	D	D	E	K	I	L	S	Y	S	L	K	P	N	Q	-	-	-	342			
Sc_Est2p	253	Y	V	S	I	L	N	S	I	C	P	P	L	E	G	T	V	L	D	L	S	H	L	S	R	Q	S	P	K	E	R	-	-	-	282			
Ea_p123	309	F	N	Y	Y	L	T	K	S	C	P	L	P	E	N	W	R	E	R	K	Q	K	I	E	N	L	I	N	K	T	R	E	E	K	341			
Sp_Tip1p	343	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	V	F	A	F	L	R	S	I	L	V	R	V	F	P	K	L	359		
Sc_Est2p	283	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	V	L	K	F	I	I	V	I	L	Q	K	L	L	P	Q	E	M	299	
Ea_p123	342	S	K	Y	Y	E	E	L	F	S	Y	T	T	D	N	K	C	V	T	Q	F	I	N	E	F	F	Y	N	I	L	P	K	D	F	374			
Sp_Tip1p	360	W	G	N	Q	R	I	F	E	I	I	L	K	D	L	E	T	F	L	K	L	S	R	Y	E	S	F	S	L	H	Y	L	M	S	392			
Sc_Est2p	300	F	G	S	K	K	N	K	G	K	I	I	K	N	L	N	L	L	S	L	P	L	N	G	Y	L	P	F	D	S	L	L	K	332				
Ea_p123	375	L	T	G	-	R	N	R	K	N	F	Q	K	K	V	K	K	Y	V	E	L	N	K	H	E	L	I	H	K	N	L	L	E	406				
Sp_Tip1p	393	N	I	K	I	S	E	I	E	W	L	V	L	G	K	R	S	N	A	K	M	C	L	S	D	F	E	K	R	K	Q	I	F	A	425			
Sc_Est2p	333	K	L	R	L	K	D	F	R	W	L	F	I	S	-	-	-	-	-	-	D	I	W	F	T	K	H	N	F	E	N	L	N	Q	L	A	I	362
Ea_p123	407	K	I	N	T	R	E	I	S	W	M	Q	V	E	T	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	437		

FIG. 64B

+



A.

Sp_Tip1p	426	E	F	I	Y	W	L	Y	N	S	F	I	P	I	L	Q	S	F	F	Y	I	T	E	S	S	D	L	R	N	R	I	T	V	Y	458
Sc_Est2p	363	C	F	I	S	W	L	F	R	Q	L	I	P	K	I	Q	T	F	F	Y	C	T	E	I	S	S	T	V	T	-	I	V	Y	394	
Ea_p123	438	K	L	L	R	W	I	F	E	D	L	V	V	S	L	I	R	C	F	F	Y	V	T	E	Q	Q	K	S	Y	S	K	I	Y	470	
Sp_Tip1p	459	F	R	K	D	I	W	K	L	L	C	R	P	F	I	T	S	M	K	M	E	A	F	E	K	I	N	N	V	R	M	D	491		
Sc_Est2p	395	F	R	H	D	T	W	N	K	L	I	T	P	F	I	V	E	Y	E	K	T	Y	L	V	E	N	N	V	C	R	N	H	N	S	427
Ea_p123	471	Y	R	K	N	I	W	D	V	I	M	K	M	S	I	A	D	L	K	K	E	T	L	A	E	V	Q	E	K	E	V	E	E	W	503
Sp_Tip1p	492	T	Q	K	T	T	L	P	P	A	V	I	R	L	L	P	K	K	-	-	N	T	F	R	L	I	T	N	L	R	K	R	F	L	522
Sc_Est2p	428	Y	T	L	S	N	F	N	H	S	K	M	R	I	I	P	K	K	S	N	N	E	F	R	I	I	A	I	P	C	R	G	A	D	460
Ea_p123	504	K	K	S	L	G	F	A	P	G	K	L	R	L	I	P	K	K	-	-	T	T	F	R	P	I	M	T	F	N	K	K	I	V	534
Sp_Tip1p	523	I	K	M	G	S	N	K	K	M	L	V	S	T	N	Q	T	L	R	P	V	A	S	I	L	K	H	L	I	N	E	-	-	-	552
Sc_Est2p	461	E	E	E	-	-	F	T	I	Y	K	E	N	H	K	N	A	I	Q	P	T	Q	K	I	L	E	Y	L	R	N	K	R	P	T	491
Ea_p123	535	N	S	D	-	-	R	K	T	T	K	L	T	T	N	T	K	L	L	N	S	H	L	M	L	K	T	L	K	N	R	-	M	F	564
Sp_Tip1p	553	E	S	S	G	I	P	F	N	L	E	V	Y	M	K	L	L	T	F	K	K	D	L	L	K	H	R	M	F	G	R	-	K	K	584
Sc_Est2p	492	S	F	T	K	I	Y	S	P	T	Q	I	A	D	R	I	K	E	F	K	Q	R	L	L	K	K	F	N	N	V	L	P	E	L	524
Ea_p123	565	K	D	P	F	G	F	A	V	F	N	Y	D	V	M	K	K	Y	E	E	F	V	C	K	W	K	V	G	Q	P	K	L	597		
Sp_Tip1p	585	Y	F	V	R	I	D	I	K	S	C	Y	D	R	I	K	Q	D	L	M	F	R	I	V	K	K	L	K	D	P	E	-	F	616	
Sc_Est2p	525	Y	F	M	K	F	D	V	K	S	C	Y	D	S	I	P	R	M	E	C	M	R	I	L	K	D	A	L	K	N	E	N	G	F	557
Ea_p123	598	F	F	A	T	M	D	I	E	K	C	Y	D	S	V	N	R	E	K	L	S	T	F	L	K	T	T	K	L	L	S	S	D	F	630
Sp_Tip1p	617	V	I	R	K	Y	A	T	I	H	A	T	S	D	R	A	T	K	N	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	634
Sc_Est2p	558	F	V	R	S	Q	Y	F	F	N	T	N	T	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	570
Ea_p123	631	W	I	M	T	A	Q	I	L	K	R	K	N	I	V	I	D	S	K	N	F	R	K	K	E	M	K	D	Y	F	R	Q	K	663	

FIG. 64C

+



A.

Sp_Tip1p	635	F	V	S	E	A	F	S	Y	F	D	M	V	P	F	E	K	V	V	Q	L	L	S	-	-	M	K	T	S	D	T	L	F	V	665	
Sc_Est2p	571	-	-	-	-	-	-	-	-	-	-	-	V	L	K	L	F	N	V	V	N	A	S	R	-	-	V	P	K	P	Y	E	L	Y	I	591
Ea_p123	664	F	Q	K	I	A	L	E	G	G	Q	Y	P	T	L	F	S	V	L	E	N	E	Q	N	D	L	N	A	K	T	L	I	V	696		
Sp_Tip1p	666	D	F	V	D	Y	W	T	K	S	S	S	E	I	F	K	M	L	K	E	H	L	S	G	H	I	V	K	I	G	N	S	Q	Y	698	
Sc_Est2p	592	D	N	V	R	T	V	H	L	S	N	Q	D	V	I	N	V	V	E	M	E	I	F	K	T	A	L	W	V	E	D	K	C	Y	624	
Ea_p123	697	E	A	K	Q	R	N	Y	F	K	K	D	N	L	L	Q	P	V	I	N	I	C	Q	Y	N	Y	I	N	F	N	G	K	F	Y	729	
Sp_Tip1p	699	L	Q	K	V	G	I	P	Q	G	S	I	L	S	S	F	L	C	H	F	Y	M	E	D	L	I	D	E	Y	L	S	F	T	K	731	
Sc_Est2p	625	I	R	E	D	G	L	F	Q	G	S	S	L	S	A	P	I	V	D	L	V	Y	D	D	L	L	E	F	Y	S	E	F	K	A	657	
Ea_p123	730	K	Q	T	K	G	I	P	Q	G	L	C	V	S	S	I	L	S	S	F	Y	A	T	L	E	E	S	S	L	G	F	L	R	762		
Sp_Tip1p	732	K	K	G	-	-	-	-	-	-	-	-	S	V	L	L	R	V	V	D	D	F	L	F	I	T	V	N	K	K	D	A	K	K	756	
Sc_Est2p	658	S	P	S	Q	D	-	-	-	-	-	-	T	L	I	L	K	L	A	D	D	F	L	I	I	S	T	D	Q	Q	V	I	N	684		
Ea_p123	763	D	E	S	M	N	P	E	N	P	N	V	N	L	L	M	R	L	T	D	D	Y	L	L	I	T	T	Q	E	N	N	A	V	L	795	
Sp_Tip1p	757	F	L	N	L	S	L	R	G	F	E	K	H	N	F	S	T	S	L	E	K	T	V	I	N	F	E	N	S	N	G	-	-	-	786	
Sc_Est2p	685	I	K	K	L	A	M	G	G	F	Q	K	Y	N	A	K	A	N	R	D	K	I	L	A	V	S	S	Q	S	D	-	-	-	713		
Ea_p123	796	F	I	E	K	L	I	N	V	S	R	E	N	G	F	K	F	N	M	K	L	Q	T	S	E	P	L	S	P	S	K	F	A	828		
Sp_Tip1p	787	-	-	-	I	I	N	N	T	F	F	N	E	S	K	K	R	M	P	F	F	G	F	S	V	N	M	R	S	L	D	T	L	L	816	
Sc_Est2p	714	-	-	-	D	D	T	V	I	Q	E	C	A	-	-	M	H	I	F	V	K	E	L	E	V	W	K	H	S	S	T	M	739			
Ea_p123	829	K	Y	G	M	D	S	V	E	E	Q	N	I	V	Q	D	Y	C	D	W	I	G	I	S	I	D	M	K	T	L	A	L	M	P	861	
Sp_Tip1p	817	A	C	P	K	I	D	E	A	L	F	N	S	T	S	V	E	L	T	K	H	M	G	K	S	F	F	Y	K	I	L	R	S	S	849	
Sc_Est2p	740	N	N	F	H	I	R	S	K	S	S	K	G	I	F	R	S	L	I	A	L	F	N	T	R	I	S	Y	K	T	I	D	T	N	772	
Ea_p123	862	N	I	N	L	R	I	E	G	I	L	C	T	L	N	L	N	M	Q	T	K	K	A	S	M	W	L	K	K	L	K	S	F	894		

FIG. 64D



72/103

A.

Sp_Tip1p	850	L	A	S	F	A	Q	V	F	I	D	I	T	H	N	S	K	F	N	S	C	C	N	I	Y	R	L	G	Y	S	M	C	M	R	882	
Sc_Est2p	773	L	N	S	T	N	T	V	L	M	Q	I	D	H	V	V	K	N	I	S	E	C	-	-	-	-	-	-	-	-	-	-	-	-	-	793
Ea_p123	895	L	M	N	N	I	T	H	Y	F	R	K	T	I	T	T	E	D	F	A	N	K	T	L	N	K	L	F	I	S	G	G	Y	K	927	
Sp_Tip1p	883	A	Q	A	Y	L	K	R	M	K	D	I	F	I	P	Q	R	M	F	I	T	D	L	L	N	V	I	G	R	K	I	W	K	K	915	
Sc_Est2p	794	-	-	-	Y	K	S	A	F	K	D	L	S	I	N	-	-	V	T	Q	N	M	Q	F	H	S	F	L	Q	R	I	I	E	M	821	
Ea_p123	928	Y	M	Q	C	A	K	E	Y	K	D	H	F	K	K	N	L	A	M	S	S	M	I	D	L	E	V	S	K	I	I	Y	S	V	960	
Sp_Tip1p	916	L	A	E	I	L	G	Y	T	S	R	R	F	L	S	S	A	E	V	K	W	L	F	C	L	G	M	R	D	G	L	K	P	S	948	
Sc_Est2p	822	T	V	S	G	C	P	I	T	K	C	D	P	L	I	E	Y	E	V	R	F	T	I	L	N	G	F	L	E	S	L	S	S	N	854	
Ea_p123	961	T	R	A	F	F	K	Y	L	V	C	N	I	K	D	T	I	F	G	E	E	H	Y	P	D	F	F	L	S	T	L	K	H	F	993	
Sp_Tip1p	949	F	K	Y	H	P	C	F	E	Q	L	I	Y	Q	F	Q	S	L	T	D	L	I	K	P	L	R	P	V	L	R	Q	V	L	F	981	
Sc_Est2p	855	T	S	-	-	-	-	-	-	-	-	-	-	-	-	K	F	K	D	N	I	L	L	R	K	E	I	Q	H	L	Q	A	Y	I	877	
Ea_p123	994	I	E	I	F	S	-	-	-	-	-	-	-	-	-	T	K	K	Y	I	E	N	R	V	C	M	I	L	K	A	K	E	A	K	1023	
Sp_Tip1p	982	L	H	R	R	I	A	D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	988		
Sc_Est2p	878	I	Y	I	H	I	V	N	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	884		
Ea_p123	1024	Q	S	L	I	Q	Y	D	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1031		

FIG. 64E



B.			
Sp_Tip1p	1	- - - - -	MTEHHTPKSRILRFLENQYVYLCT 24
Sc_Est2p	1	- - - - -	- - - - - MKILFEF 7
Ea_p123	1	MEVDVDNQADNHG	HSALKTCEEIKEAKTLYSW 33
Sp_Tip1p	25	LNDYVQLVLRGSPA	SSY SNICERLRSDVQTSFS 57
Sc_Est2p	8	IQDKLDIDLQTN	- - STYK - - ENLKCGHFNGLD 35
Ea_p123	34	IQKVIRCRNQSQ	- - SHYK - - DLEDIKIFAQTN 61
Sp_Tip1p	58	IFLHSTVVGFDSP	DEGVQFSSPKCSQSELIAN 90
Sc_Est2p	36	EILTTTCFALPNSR	- KIA L PCLPGDLSHKAVIDH 67
Ea_p123	62	I V A T P R D Y N E E D F K V I A R K E V F S T G L M I E L I D K	94
Sp_Tip1p	91	VVKQMFDESFERR	- NLLMKGF F S M N H E D F R A M H 122
Sc_Est2p	68	C I I Y L L T G E L Y N	- - N V L T F G Y K I A R N E D - - - - 93
Ea_p123	95	C L V E L L S S S D V S D R Q K L Q C F G F Q L K G N Q	- - - - 122
Sp_Tip1p	123	VNGVQNDLVSTFPN	Y L I S I L E S K N W Q L L L E I I G 155
Sc_Est2p	94	- - - V N N S L F C H S A N V N V T L L K G A A W K M F H S L V G	123
Ea_p123	123	- - - L A K T H L L T A L S T Q K Q Y F F Q D E W N Q V R A M I G	152
Sp_Tip1p	156	S D A M H Y L L S K G S I F E A L P N D N Y L Q I S G I P L F K N	188
Sc_Est2p	124	T Y A F V D L L I N Y T V I Q F N - G Q F F T Q I V G N R C N E P	155
Ea_p123	153	N E L F R H L Y T K Y L I F Q R T S E G T L V Q F C G N N V F D H	185
Sp_Tip1p	189	N V F E E T V S K K R K R T I E T S I T Q N	- - - K S A R K E V S 218
Sc_Est2p	156	H L P P K W V Q	- - R S S S S A T A A Q I - - - K Q L T E P V T 183
Ea_p123	186	L K V N D K F D K - K Q K G G A A D M N E P R C C S T C K Y N V K	217

FIG. 64F



B.

Sp_Tip1p	219	WNSISISRFSIFYRSSYKKFKQDLYFNLHSICD	251
Sc_Est2p	184	N-----KQFLHKLNINSSSFFP	200
Ea_p123	218	NEK--DHFLNNINVPNWNMKSRTIFYCTHFN	248
Sp_Tip1p	252	RNTVHMWLQWIFPRQFGLINAFQVKQLHKVIPL	284
Sc_Est2p	201	-----YSKILPSSS--SIKKLTDLREAIFF	223
Ea_p123	249	R-----NNQFFKKHEFVSNKNNISAMDRAQTI	275
Sp_Tip1p	285	VS-----QSTVVPKRLLKVYPLIEQTAKRRLHRIS	313
Sc_Est2p	224	TN-----LVKIPQRLKVRINLTQKLLKRHKRLN	252
Ea_p123	276	FTNIFRFNRIRKKLKDKVIEKIAYMLEKVKDFN	308
Sp_Tip1p	314	LSKVYNHYCPYID-THDDEKILSYSLKPNQ---	342
Sc_Est2p	253	YVSI LNSICPPLEGTVDLSHL SRQSPKER---	282
Ea_p123	309	FNYYLT KSCPLPENWRERKQKIENLINKTREEK	341
Sp_Tip1p	343	-----VFALRSILVRVFPKLI	359
Sc_Est2p	283	-----VLKFIIVILQKLLPQEM	299
Ea_p123	342	SKYYEELFSYTTDNKCVTTQFIN EFFYNILPKDF	374
Sp_Tip1p	360	WGNQRIFEIILKDL ETFLKL SRYESFSLHYLMS	392
Sc_Est2p	300	FGSKKNKGKIIKNNLNL LSLPLNGYLPFD SLLK	332
Ea_p123	375	LTG-RNRKNFQK KVKKYVELNKH ELIHKNNLLE	406
Sp_Tip1p	393	NIKISEIEWLVLGKRSNAKMCLSDFEKRKQIFA	425
Sc_Est2p	333	KLRLKDFRWLFIS--DIWFTKHNFENLNQLAI	362
Ea_p123	407	KINTREISWMQVETS-AKH FYFDHEN-IYVLW	437

FIG. 64G



B.

Sp_Tip1p	426	EF	I	Y	W	L	Y	N	S	F	I	I	P	I	L	Q	S	F	F	Y	I	T	E	S	S	D	L	R	N	R	T	V	Y	458	
Sc_Est2p	363	C	F	I	S	W	L	F	R	Q	L	I	P	K	I	Q	T	F	F	Y	C	T	E	I	S	S	T	V	T	-	I	V	Y	394	
Ea_p123	438	K	L	L	R	W	I	F	E	D	L	V	S	L	I	R	C	F	F	Y	V	T	E	Q	Q	K	S	Y	S	K	T	Y	470		
Sp_Tip1p	459	F	R	K	D	I	W	K	L	L	C	R	P	F	I	T	S	M	K	M	E	A	F	E	K	I	N	E	N	N	V	R	M	D	491
Sc_Est2p	395	F	R	H	D	T	W	N	K	L	I	T	P	F	I	V	E	Y	F	K	T	Y	L	V	E	N	N	V	C	R	N	H	N	S	427
Ea_p123	471	Y	R	K	N	I	W	D	V	I	M	K	M	S	I	A	D	L	K	K	E	T	L	A	E	V	Q	E	K	E	V	E	W	503	
Sp_Tip1p	492	T	Q	K	T	T	L	P	P	A	V	I	R	L	L	P	K	K	-	-	N	T	F	R	L	I	T	N	L	R	K	R	F	L	522
Sc_Est2p	428	Y	T	L	S	N	F	N	H	S	K	M	R	I	I	P	K	K	S	N	N	E	F	R	I	I	A	I	P	C	R	G	A	D	460
Ea_p123	504	K	K	S	L	G	F	A	P	G	K	L	R	L	I	P	K	K	-	-	T	T	F	R	P	I	M	T	F	N	K	K	I	V	534
Sp_Tip1p	523	I	K	M	G	S	N	K	K	M	L	V	S	T	N	Q	T	L	R	P	V	A	S	I	L	K	H	L	I	N	E	-	-	-	552
Sc_Est2p	461	E	E	E	-	-	F	T	I	Y	K	E	N	H	K	N	A	I	Q	P	T	Q	K	I	L	E	Y	L	R	N	K	R	P	T	491
Ea_p123	535	N	S	D	-	-	R	K	T	T	K	L	T	T	N	T	K	L	L	N	S	H	L	M	L	K	T	L	K	N	R	-	M	F	564
Sp_Tip1p	553	E	S	S	G	I	P	F	N	L	E	V	Y	M	K	L	L	T	F	K	K	D	L	L	K	H	R	M	F	G	R	-	K	K	584
Sc_Est2p	492	S	F	T	K	I	Y	S	P	T	Q	I	A	D	R	I	K	E	F	K	Q	R	L	L	K	K	F	N	N	V	L	P	E	L	524
Ea_p123	565	K	D	P	F	G	F	A	V	F	N	Y	D	D	V	M	K	K	Y	E	E	F	V	C	K	W	K	Q	V	G	Q	P	K	L	597
Sp_Tip1p	585	Y	F	V	R	I	D	I	K	S	C	Y	D	R	I	K	Q	D	L	M	F	R	I	V	K	K	K	L	K	D	P	E	-	F	616
Sc_Est2p	525	Y	F	M	K	F	D	V	K	S	C	Y	D	S	I	P	R	M	E	C	M	R	I	L	K	D	A	L	K	N	E	N	G	F	557
Ea_p123	598	F	F	A	T	M	D	I	E	K	C	Y	D	S	V	N	R	E	K	L	S	T	F	L	K	T	T	K	L	L	S	S	D	F	630
Sp_Tip1p	617	V	I	R	K	Y	A	T	I	H	A	T	S	D	R	A	T	K	N	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	634
Sc_Est2p	558	F	V	R	S	Q	Y	F	F	N	T	N	T	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	570	
Ea_p123	631	W	I	M	T	A	Q	I	L	K	R	K	N	I	V	I	D	S	K	N	F	R	K	K	E	M	K	D	Y	F	R	Q	K	663	

FIG. 64H

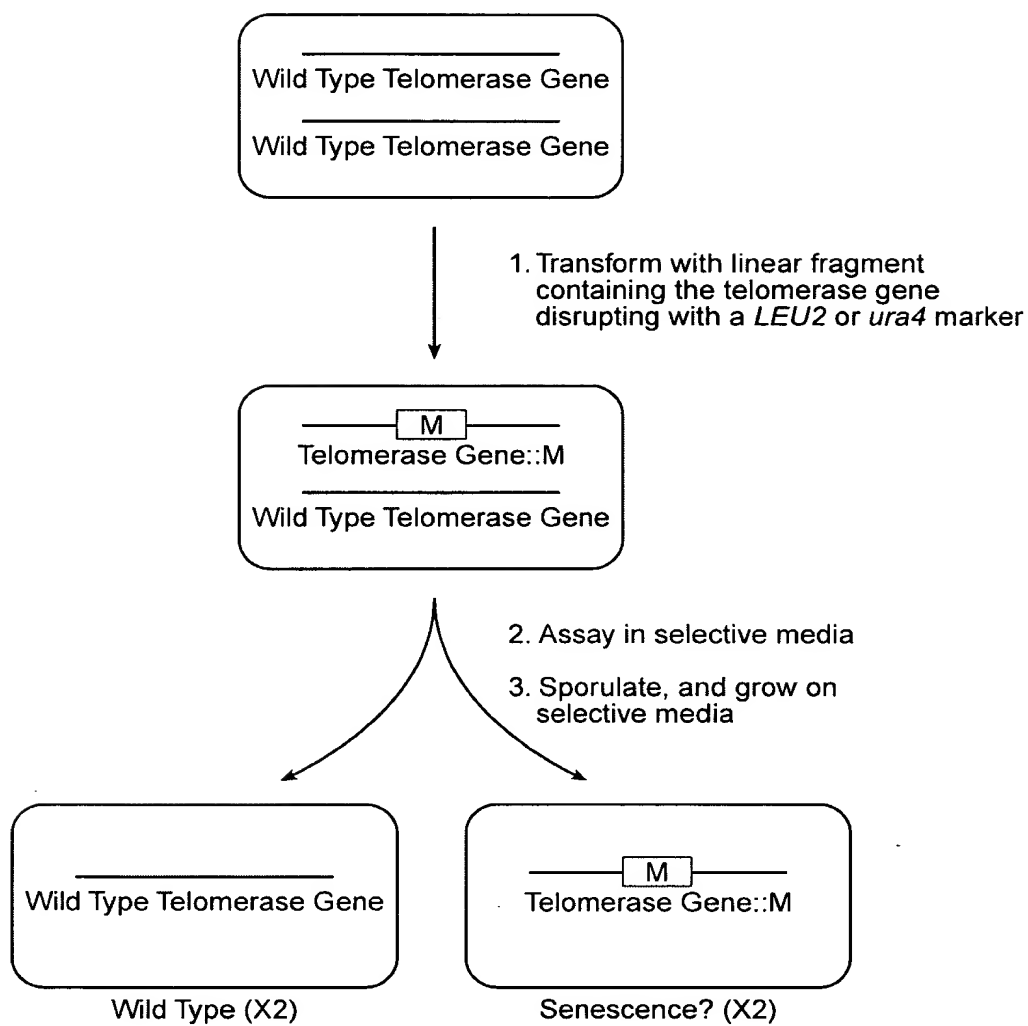


77/103

B.

Sp_Tip1p	850	L	A	S	F	A	Q	V	F	I	D	I	T	H	N	S	K	F	N	S	C	C	N	I	Y	R	L	G	Y	S	M	C	M	R		882	
Sc_Est2p	773	L	N	S	T	N	T	V	L	M	Q	I	D	H	V	V	K	N	I	S	E	C	-	-	-	-	-	-	-	-	-	-	-	-	-	-	793
Ea_p123	895	L	M	N	N	I	T	H	Y	F	R	K	T	I	T	T	E	D	F	A	N	K	T	L	N	K	L	F	I	S	G	G	Y	K		927	
Sp_Tip1p	883	A	Q	A	Y	L	K	R	M	K	D	I	F	I	P	Q	R	M	F	I	T	D	L	L	N	V	I	G	R	K	I	W	K	K		915	
Sc_Est2p	794	-	-	-	Y	K	S	A	F	K	D	L	S	I	N	-	-	V	T	Q	N	M	Q	F	H	S	F	L	Q	R	I	I	E	M		821	
Ea_p123	928	Y	M	Q	C	A	K	E	Y	K	D	H	F	K	K	N	L	A	M	S	S	M	I	D	L	E	V	S	K	I	I	Y	S	V		960	
Sp_Tip1p	916	L	A	E	I	L	G	Y	T	S	R	R	F	L	S	S	A	E	V	K	W	L	F	C	L	G	M	R	D	G	L	K	P	S		948	
Sc_Est2p	822	T	V	S	G	C	P	I	T	K	C	D	P	L	I	E	Y	E	V	R	F	T	I	L	N	G	F	L	E	S	L	S	S	N		854	
Ea_p123	961	T	R	A	F	F	K	Y	L	V	C	N	I	K	D	T	I	F	G	E	E	H	Y	P	D	F	F	L	S	T	L	K	H	F		993	
Sp_Tip1p	949	F	K	Y	H	P	C	F	E	Q	L	I	Y	Q	F	Q	S	L	T	D	L	I	K	P	L	R	P	V	L	R	Q	V	L	F		981	
Sc_Est2p	855	T	S	-	-	-	-	-	-	-	-	-	-	-	-	K	F	K	D	N	I	I	L	L	R	K	E	I	Q	H	L	Q	A	Y	I		877
Ea_p123	994	I	E	I	F	S	-	-	-	-	-	-	-	-	-	T	K	K	Y	I	F	N	R	V	C	M	I	L	K	A	K	E	A	K		1023	
Sp_Tip1p	982	L	H	R	R	I	A	D	-																											988	
Sc_Est2p	878	I	Y	I	H	I	V	N	-																											884	
Ea_p123	1024	Q	S	L	I	Q	Y	D	A																											1031	

FIG. 64J



(These cells will show a senescence phenotype if the disrupted gene encodes a telomerase subunit.)

FIG. 65

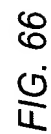


FIG. 66

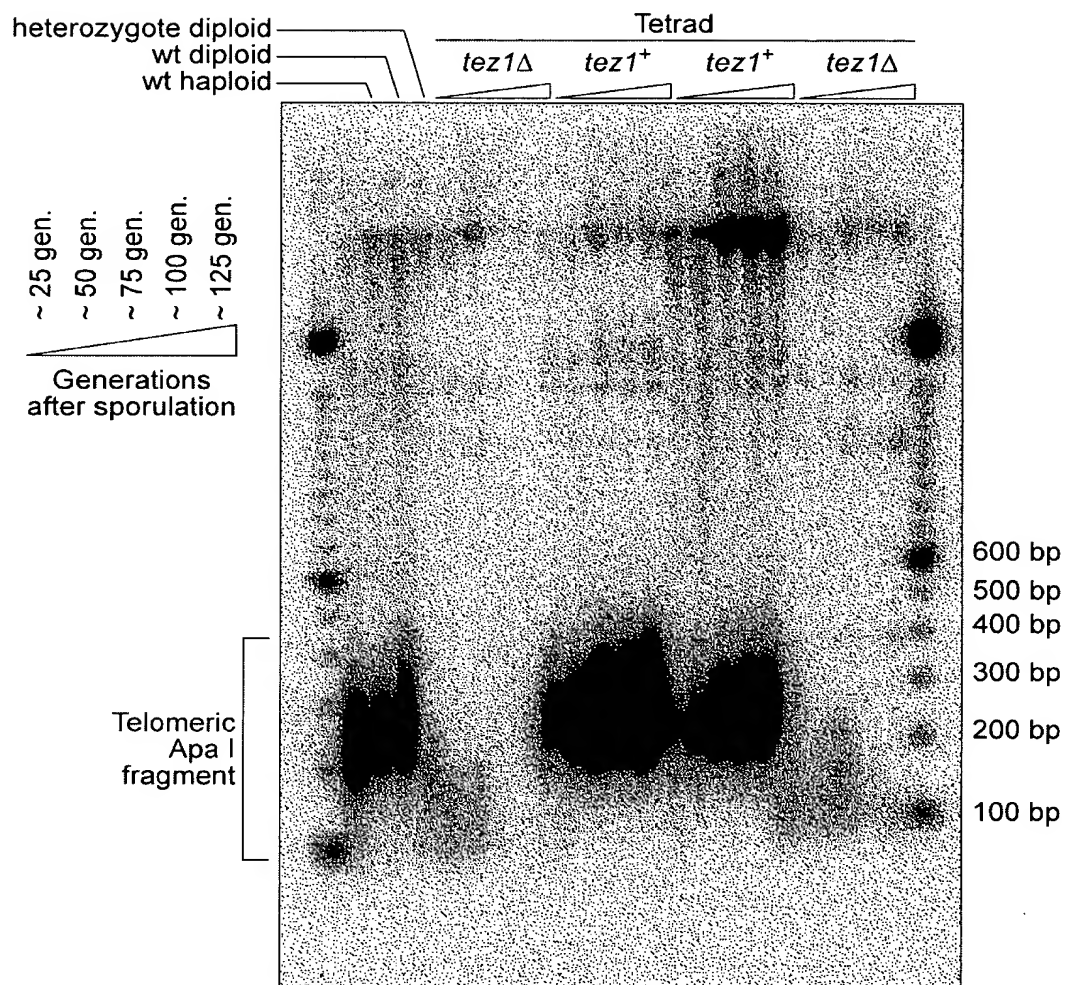


FIG. 67



81/103

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      1
GCCAAGTTCCTGCACTGGCTG  met ser val tyr val val glu leu leu
                        ATG AGT GTG TAC GTC GTC GAG CTG CTC

    10                                20
arg ser phe phe tyr val thr glu thr thr phe gln lys asn arg
AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC AGG

                                30
leu phe phe tyr arg lys ser val trp ser lys leu gln ser ile
CTC TTT TTC TAC CGG AAG AGT GTC TGG AGC AAG TTG CAA AGC ATT

    40                                50
gly ile arg gln his leu lys arg val gln leu arg glu leu ser
GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG TCG

                                60
glu ala glu val arg gln his arg glu ala arg pro ala leu leu
GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG CTG

    70                                80
thr ser arg leu arg phe ile pro lys pro asp gly leu arg pro
ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG CCG

                                90
ile val asn met asp tyr val val gly ala arg thr phe arg arg
ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC AGA

    100                                110
glu lys      ala glu arg leu thr ser arg val lys ala leu phe
GAA AAG ARG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG TTC

                                120
ser val leu asn tyr glu arg ala arg arg pro gly leu leu gly
AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC GGC CTC CTG GGC

    130                                140
ala ser val leu gly leu asp asp ile his arg ala trp arg thr
GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC ACC

                                150
phe val leu arg val arg ala gln asp pro pro pro glu leu tyr
TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG CTG TAC

    160                                170
phe val lys val asp val thr gly ala tyr asp thr ile pro gln
TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC CAG

                                180
asp arg leu thr glu val ile ala ser ile ile lys pro gln asn
GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG AAC

    190                                200
thr tyr cys val arg arg tyr ala val val gln lys ala ala met
ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC ATG

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FIG. 68A



82/103

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                210
gly thr ser ala arg pro ser arg ala thr ser tyr val gln cys
GGC ACG TCC GCA AGG CCT TCA AGA GCC ACG TCC TAC GTC CAG TGC

220                230
gln gly ile pro gln gly ser ile leu ser thr leu leu cys ser
CAG GGG ATC CCG CAG GGC TCC ATC CTC TCC ACG CTG CTC TGC AGC

                240
leu cys tyr gly asp met glu asn lys leu phe ala gly ile arg
CTG TGC TAC GGC GAC ATG GAG AAC AAG CTG TTT GCG GGG ATT CGG

250                260
arg asp gly leu leu leu arg leu val asp asp phe leu leu val
CGG GAC GGG CTG CTC CTG CGT TTG GTG GAT GAT TTC TTG TTG GTG

                270
thr pro his leu thr his ala lys thr phe leu arg thr leu val
ACA CCT CAC CTC ACC CAC GCG AAA ACC TTC CTC AGG ACC CTG GTC

280                290
arg gly val pro glu tyr gly cys val val asn leu arg lys thr
CGA GGT GTC CCT GAG TAT GGC TGC GTG GTG AAC TTG CGG AAG ACA

                300
val val asn phe pro val glu asp glu ala leu gly gly thr ala
GTG GTG AAC TTC CCT GTA GAA GAC GAG GCC CTG GGT GGC ACG GCT

310                320
phe val gln met pro ala his gly leu phe pro trp cys gly leu
TTT GTT CAG ATG CCG GCC CAC GGC CTA TTC CCC TGG TGC GGC CTG

                330
leu leu asp thr arg thr leu glu val gln ser asp tyr ser ser
CTG CTG GAT ACC CGG ACC CTG GAG GTG CAG AGC GAC TAC TCC AGC

340                350
tyr ala arg thr ser ile arg ala ser leu thr phe asn arg gly
TAT GCC CGG ACC TCC ATC AGA GCC AGT CTC ACC TTC AAC CGC GGC

                360
phe lys ala gly arg asn met arg arg lys leu phe gly val leu
TTC AAG GCT GGG AGG AAC ATG CGT CGC AAA CTC TTT GGG GTC TTG

370                380
arg leu lys cys his ser leu phe leu asp leu gln val asn ser
CGG CTG AAG TGT CAC AGC CTG TTT CTG GAT TTG CAG GTG AAC AGC

                390
leu gln thr val cys thr asn ile tyr lys ile leu leu leu gln
CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG CTG CAG

400                410
ala tyr arg phe his ala cys val leu gln leu pro phe his gln
GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT CAT CAG

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FIG. 68B



83/103

420
gln val trp lys asn pro his phe ser cys ala ser ser leu thr
CAA GTT TGG AAG AAC CCA CAT TTT TCC TGC GCG TCA TCT CTG ACA

430
arg leu pro leu leu leu his pro glu ser gln glu arg arg asp
CGG CTC CCT CTG CTA CTC CAT CCT GAA AGC CAA GAA CGC AGG GAT

440
450
val ala gly gly gln gly arg arg arg pro ser ala leu arg gly
GTC GCT GGG GGC CAA GGG CGC CGC CGG CCC TCT GCC CTC CGA GGC

460
arg ala val ala val pro pro ser ile pro ala gln ala asp ser
CGT GCA GTG GCT GTG CCA CCA AGC ATT CCT GCT CAA GCT GAC TCG

470
480
thr pro cys his leu arg ala thr pro gly val thr gln asp ser
ACA CCG TGT CAC CTA CGT GCC ACT CCT GGG GTC ACT CAG GAC AGC

490
pro asp ala ala glu ser glu ala pro gly asp asp ala asp cys
CCA GAC GCA GCT GAG TCG GAA GCT CCC GGG GAC GAC GCT GAC TGC

500
510
pro gly gly arg ser gln pro gly thr ala leu arg leu gln asp
CCT GGA GGC CGC AGC CAA CCC GGC ACT GCC CTC AGA CTT CAA GAC

520
his pro gly leu met ala thr arg pro gln pro gly arg glu gln
CAT CCT GGA CTG ATG GCC ACC CGC CCA CAG CCA GGC CGA GAG CAG

530
540
thr pro ala ala leu ser arg arg ala tyr thr ser gln gly gly
ACA CCA GCA GCC CTG TCA CGC CGG GCT TAT ACG TCC CAG GGA GGG

550
arg gly gly pro his pro gly leu his arg trp glu ser glu ala
AGG GGC GGC CCA CAC CCA GGC CTG CAC CGC TGG GAG TCT GAG GCC

560
564
OP
TGA GTGAGTGTGTTGGCCGAGGCCTGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGC
CTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTCCAGCACACCTGCGTTTTCACTTCCCCAC
AGGCTGGCGTTTCGGTCCACCCCAGGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACT
CCCCACATAGGAATAGTCCATCCCCAGATTGCGCCATTGTTTACCCTTCGCCCTGCCTTCC
TTTGCCTTCCACCCCCACCATTTCAGGTGGAGACCCTGAGAAGGACCCTGGGAGCTTTGGG
AATTTGGAGTGACCAAAGGTGTGCCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGG
GTCCCTGTGGGTCAAATTGGGGGGAGGTGCTGTGGGAGTAAATACTGAATATATGAGTT
TTTCAGTTTTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIG. 68C



Motif -1
 Ep p123 ...LVVSLIRCFYVTEQOKSYSKT...
 Sp Tez1 ...FIIPILQSFFYITESSDLRNRT...
 Sc Est2 ...LIPKIIQTFFYCTEISSTVTIV...
 Hs TCP1 ...YVVELLRSFFYVTETTFQKNRL...
 consensus FFY TE

Motif 0
 Ep p123 ...KSLGFAPGKLRLIPKKT--TFRPIMTFNKKIV...
 Sp Tez1 ...QKTTLPPAVIRLLPKKN--TFLITNLKRFL...
 Sc Est2 ...TLSNFNHSMRIIPKKSNNEFRIIAIPCRGAD...
 Hs TCP1 ...ARPALLTSRLRFIPKPD--GLRPIVNMDYVVG...
 consensus R PK R I

Motif A
 Ep p123 ...PKLFFATMDIEKCYDSVNREKLSTFLK...
 Sp Tez1 ...RKKYFVRIDIKSCYDRIKQDLMFRIVK...
 Sc Est2 ...PELYFMKFVDKSCYDSIPRMECMRILK...
 Hs TCP1 ...PELYFVKVDVTGAYDTIPQDRLTEVIA...//...
 consensus F D YD

Motif B
 Ep p123 ...NGKFYKQTKGIPQGLCVSSILSSFYYA...
 Sp Tez1 ...GNSQYLQKVGIPQGSILSSFCHFYME...
 Sc Est2 ...EDKCYIREDGLFQGSSLSAPIVDLVYD...
 Hs TCP1 ...RATSYVQCQGIPQGSILSTLLCSLCYG...
 consensus G QG S

Motif C
 Ep p123 ...PNVNLLMRLTDDYLLITTQENN...
 Sp Tez1 ...KKGSVLLRVDDFLFITVNKKD...
 Sc Est2 ...SQDTLILKLADDFLIISTDQQQ...
 Hs TCP1 ...RRDGLLLRLVDDFLLVTPHLTH...
 consensus DD L

Motif D
 Ep p123 ...NVSRENGFKFNMKKL...
 Sp Tez1 ...LNLSLRGFKEHNFST...
 Sc Est2 ...KKLAMGGFQKYNKA...
 Hs TCP1 ...LRTLVRGVPEYGCVV...
 consensus G

FIG. 69

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85/103

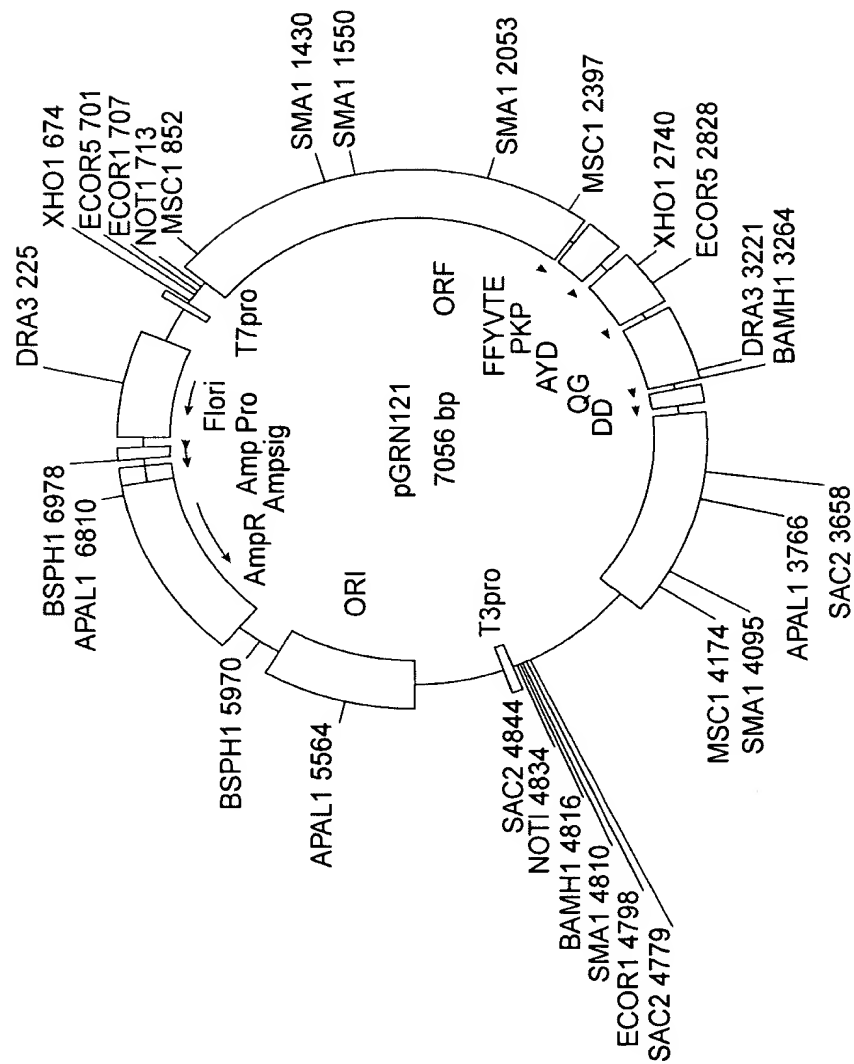


FIG. 70

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1	GCAGCGCTGC	GTCTGCTGC	GCACGTGGGA	AGCCCTGGCC	CCGGCCACCC
51	CCGCGATGCC	GCGCGCTCCC	CGTGCCGAG	CCGTGCGCTC	CCTGCTGCGC
101	AGCCACTACC	GCGAGGTGCT	GCCGCTGGCC	ACGTTCGTGC	GGCGCCTGGG
151	GCCCCAGGGC	TGGCGGCTGG	TGCAGCGCGG	GGACCCGGCG	GCTTTCGCGC
201	CGNTGGTGGC	CCANTGCNTG	GTGTGCGTGC	CCTGGGANGN	ANGGCNCCCC
251	CCCGCCGCCC	CCTCCTTCCG	CCAGGTGTCC	TGCCTGAANG	ANCTGGTGGC
301	CCGAGTGCTG	CANANGCTGT	GCGANCGCGG	CGCGAANAAC	GTGCTGGCCT
351	TCGGCTTCGC	GCTGCTGGAC	GGGGCCCGCG	GGGGCCCCCC	CGAGGCCTTC
401	ACCACCAGCG	TGCGCAGCTA	CCTGCCCAAC	ACGGTGACCG	ACGCACTGCG
451	GGGGAGCGGG	GCGTGCGGGC	TGCTGCTGCG	CCGCGTGGGC	GACGACGTGC
501	TGGTTCACCT	GCTGGCACGC	TGCGCGNTNT	TTGTGCTGGT	GGNTCCCAGC
551	TGCGCCTACC	ANGTGTGCGG	GCCGCCGCTG	TACCAGCTCG	GCGCTGCNAC
601	TCAGGCCCGG	CCCCGCCAC	ACGCTANTGG	ACCCGAANGC	GTCTGGGATC
651	CAACGGGCCT	GGAACCATAG	CGTCAGGGAG	GCCGGGGTCC	CCCTGGGCTG
701	CCAGCCCCGG	GTGCGAGGAG	GCGCGGGGGC	AGTGCCAGCC	GAAGTCTGCC
751	GTTGCCCAAG	AGGCCCAGGC	GTGGCGCTGC	CCCTGAGCCG	GAGCGGACGC
801	CCGTGGGGCA	GGGGTCCTGG	GCCCACCCGG	GCAGGACGCC	TGGACCGAGT
851	GACCGTGGTT	TCTGTGTGGT	GTACCTGACC	AGACCCGCCG	AAGAAGCCAC
901	CTCTTTGGAG	GGTGCGCTCT	CTGGCACGCG	CCACTCCCAC	CCATCCGTGG
951	GCCGCCAGCA	CCACGCGGGC	CCCCATCCA	CATCGCGGCC	ACCACGTCTT
1001	GGGACACGCC	TTGTCCCCCG	GTGTACGCCG	AGACCAAGCA	CTTCCTCTAC
1051	TCCTCAGGCG	ACAAGNACAC	TGCGNCCCTC	CTTCCTACTC	AATATATCTG
1101	AGGCCCAGCC	TGACTGGCGT	TCGGGAGGTT	CGTGGAGACA	NTCTTTCTGG
1151	TTCCAGGCCT	TGGATGCCAG	GATTCCTCCG	AGGTTGCCCC	GCCTGCCCCA
1201	GCGNTACTGG	CAAATGCGGC	CCCTGTTTCT	GGAGCTGCTT	GGGAACACAG
1251	CGCAGTGCCC	CTACGGGGTG	TTCCTCAAGA	CGCACTGCCC	GCTGCGAGCT
1301	GCGGTACACC	CAGCAGCCGG	TGTCTGTGCC	CGGGAGAAGC	CCCAGGGCTC
1351	TGTGGCGGCC	CCCGAGGAGG	AGGAACACAG	ACCCCGTCCG	CCTGGTGCAG
1401	CTGCTCCGCC	AGCACAGCAG	CCCCTGGCAG	GTGTACGGCT	TCGTGCGGGC
1451	CTGCCCTGCG	CGGCTGGTGC	CCCCAGGCCT	CTGGGGCTCC	AGGCACAACG
1501	AACGCCGCTT	CCTCAGGAAC	ACCAAGAAGT	TCATCTCCCT	GGGGAACCAT
1551	GCCAAGCTCT	CGCTGCAGGA	GCTGACGTGG	AAGATGAGCG	TGCGGGACTG
1601	CGCTTGGCTG	CGCAGGAGCC	CAGGGGTTGG	CTGTGTTCCG	GCCGCAGAGC
1651	ACCGTCTGCG	TGAGGAGATC	CTGGCCAAGT	TCCTGCACTG	GCTGATGAGT
1701	GTGTACGTCG	TCGAGCTGCT	CAGGTCTTTC	TTTTATGTCA	CGGAGACCAC
1751	GTTTCAAAAG	AACAGGCTCT	TTTTCTACCG	GAAGAGTGTC	TGGAGCAAGT
1801	TGCAAAGCAT	TGGAATCAGA	CAGCACTTGA	AGAGGGTGCA	GCTGCGGGAG
1851	CTGTGCGAAG	CAGAGGTCAG	GCAGCATCGG	GAAGCCAGGC	CCGCCCTGCT
1901	GACGTCCAGA	CTCCGCTTCA	TCCCCAAGCC	TGACGGGCTG	CGGCCGATTG
1951	TGAACATGGA	CTACGTGCTG	GGAGCCAGAA	CGTTCCGCAG	AGAAAAGAGG
2001	GCCGAGCGTC	TCACCTCGAG	GGTGAAGGCA	CTGTTACGCG	TGCTCAACTA
2051	CGAGCGGGCG	CGGCGCCCCG	GCCTCCTGGG	CGCTCTGTG	CTGGGCCTGG
2101	ACGATATCCA	CAGGGCCTGG	CGCACCTTCG	TGCTGCGTGT	GCGGGCCAG
2151	GACCCGCCGC	CTGAGCTGTA	CTTTGTCAAG	GTGGATGTGA	CGGGCGCGTA
2201	CGACACCATC	CCCCAGGACA	GGCTCACGGA	GGTCATCGCC	AGCATCATCA
2251	AACCCAGAA	CACGTACTGC	GTGCGTCGGT	ATGCCGTGGT	CCAGAAGGCC
2301	CCCCATGGGC	ACGTCCGCAA	GGCCTTCAAG	AGCCACGTCT	CTACCTTGAC
2351	AGACCTCCAG	CCGTACATGC	GACAGTTCGT	GGCTCACCTG	CAGGANAACA
2401	GCCCGCTGAG	GGATGCCGTC	GTCATCGAGC	AGAGCTCCTC	CCTGAATGAG
2451	GCCAGCAGTG	GCCTCTTCGA	CGTCTTCCTA	CGCTTCATGT	GCCACCACGC

FIG. 71A



2501	CGTGCGCATC	AGGGGCAAGT	CCTACGTCCA	GTGCCAGGGG	ATCCCGCAGG
2551	GCTCCATCCT	CTCCACGCTG	CTCTGCAGCC	TGTGCTACGG	CGACATGGAG
2601	AACAAGCTGT	TTGCGGGGAT	TCGGCGGGAC	GGGCTGCTCC	TGCGTTTGGT
2651	GGATGATTTT	TTGTTGGTGA	CACCTCACCT	CACCCACGCG	AAAACCTTCC
2701	TCAGGACCCT	GGTCCGAGGT	GTCCCTGAGT	ATGGCTGCGT	GGTGAACCTG
2751	CGGAAGACAG	TGGTGAACCT	CCCTGTAGAA	GACGAGGCCC	TGGGTGGCAC
2801	GGCTTTTGT	CAGATGCCGG	CCCACGGCCT	ATTCCCCTGG	TGCGGCCTGC
2851	TGCTGGATAC	CCGGACCCTG	GAGGTGCAGA	GCGACTACTC	CAGCTATGCC
2901	CGGACCTCCA	TCAGAGCCAG	TCTCACCTTC	AACCGCGGCT	TCAAGGCTGG
2951	GAGGAACATG	CGTCGCAAAC	TCTTTGGGGT	CTTGCGGCTG	AAGTGTCAAC
3001	GCCTGTTTCT	GGATTTCAG	GTGAACAGCC	TCCAGACGGT	GTGCACCAAC
3051	ATCTACAAGA	TCCTCCTGCT	GCAGGCGTAC	AGGTTTCACG	CATGTGTGCT
3101	GCAGCTCCCA	TTTCATCAGC	AAGTTTGGAA	GAACCCACAC	TTTTTCCTGC
3151	GCGTCATCTC	TGACACGGCC	TCCCTCTGCT	ACTCCATCCT	GAAAGCCAAG
3201	AACGCAGGGA	TGTCGCTGGG	GGCCAAGGGC	GCCGCCGGCC	CTCTGCCCTC
3251	CGAGGCCGTG	CAGTGGCTGT	GCCACCAAGC	ATTCTGCTC	AAGCTGACTC
3301	GACACCGTGT	CACCTACGTG	CCACTCCTGG	GGTCACTCAG	GACAGCCCAG
3351	ACGCAGCTGA	GTCGGAAGCT	CCCGGGGACG	ACGCTGACTG	CCCTGGAGGC
3401	CGCAGCCAAC	CCGGCACTGC	CCTCAGACTT	CAAGACCATC	CTGGACTGAT
3451	GGCCACCCGC	CCACAGCCAG	GCCGAGAGCA	GACACCAGCA	GCCCTGTCAC
3501	GCCGGGCTCT	ACGTCCCAGG	GAGGGAGGGG	CGGCCACAC	CCAGGCCCGC
3551	ACCGCTGGGA	GTCTGAGGCC	TGAGTGAGTG	TTTGGCCGAG	GCCTGCATGT
3601	CCGGCTGAAG	GCTGAGTGTC	CGGCTGAGGC	CTGAGCGAGT	GTCCAGCCAA
3651	GGGCTGAGTG	TCCAGCACAC	CTGCCGTCTT	CACTTCCCCA	CAGGCTGGCG
3701	CTCGGCTCCA	CCCCAGGGCC	AGCTTTTCCT	CACCAGGAGC	CCGGCTTCCA
3751	CTCCCCACAT	AGGAATAGTC	CATCCCCAGA	TTCGCCATTG	TTACCCCTC
3801	GCCCTGCCCT	CCTTTGCCTT	CCACCCCCAC	CATCCAGGTG	GAGACCCCTGA
3851	GAAGGACCCT	GGGAGCTCTG	GGAATTTGGA	GTGACCAAAG	GTGTGCCCTG
3901	TACACAGGCG	AGGACCCTGC	ACCTGGATGG	GGGTCCCTGT	GGGTCAAATT
3951	GGGGGGAGGT	GCTGTGGGAG	TAAAATACTG	AATATATGAG	TTTTTCAGTT
4001	TTGAAAAAAA	AAAAAAAAAA	AAAAAAAAAA		

FIG. 71B



89/103

a P R G R R R A G S P A G T L R ? ? C A G -
b R V G D D V L V H L L A R C A ? F V L V -
c A W A T T C W F T C W H A A R ? L C W W -

541 GGNTCCCAGCTGCGCCTACCANGTGTGCGGGCCGCGCTGTACCAGCTCGGCGCTGCNAC
-----+-----+-----+-----+-----+ 600
CCNAGGGTCGACGCGGATGGTNCACACGCCCGGCGGCGACATGGTCGAGCCGCGACGNTG

a G S Q L R L P ? V R A A A V P A R R C ? -
b ? P S C A Y ? V C G P P L Y Q L G A A T -
c ? P A A P T ? C A G R R C T S S A L ? L -

601 TCAGGCCCCGCCCCGCCACACGCTANTGGACCCGAANGCGTCTGGGATCCAACGGGCGCT
-----+-----+-----+-----+-----+ 660
AGTCGGGGCGGGGCGGTGTGCGATNACCTGGGCTTNCGCAGACCCTAGGTTGCCCCGA

a S G P A P A T R ? W T R ? R L G S N G P -
b Q A R P P P H A ? G P E ? V W D P T G L -
c R P G P R H T L ? D P ? A S G I Q R A W -

661 GGAACCATAGCGTCAGGGAGGCGGGGTCCCCCTGGGCTGCCAGCCCCGGGTGCGAGGAG
-----+-----+-----+-----+-----+ 720
CCTTGGTATCGCAGTCCCTCCGGCCCCAGGGGACCCGACGGTCGGGGCCCCACGCTCCTC

a G T I A S G R P G S P W A A S P G C E E -
b E P * R Q G G R G P P G L P A P G A R R -
c N H S V R E A G V P L G C Q P R V R G G -

721 GCGCGGGGGCAGTGCCAGCCGAAGTCTGCCGTTGCCCAAGAGGCCAGGCGTGCGCTGC
-----+-----+-----+-----+-----+ 780
CGCGCCCCCGTCACGGTCGGCTTCAGACGGCAACGGGTTCTCCGGGTCCGCACCGCGACG

a A R G Q C Q P K S A V A Q E A Q A W R C -
b R G G S A S R S L P L P K R P R R G A A -
c A G A V P A E V C R C P R G P G V A L P -

781 CCCTGAGCCGAGCGGACGCCCCGTTGGGCAGGGGTCTTGGGCCACCCGGGCAGGACGCC
-----+-----+-----+-----+-----+ 840
GGGACTCGGCTCGCCTGCGGGCAACCCGTCCCCAGGACCCGGGTGGGCCCCGTCTGCGG

a P * A G A D A R W A G V L G P P G Q D A -
b P E P E R T P V G Q G S W A H P G R T P -
c L S R S G R P L G R G P G P T R A G R L -

841 TGGACCGAGTGACCGTGTTTCTGTGTGGTGTCACCTGCCAGACCCGCGGAAGAAGCCAC
-----+-----+-----+-----+-----+ 900
ACCTGGCTCACTGGCACCAAGACACACCACAGTGGACGGTCTGGGCGGCTTCTTCGGTG

a W T E * P W F L C G V T C Q T R R R S H -
b G P S D R G F C V V S P A R P A E E A T -
c D R V T V V S V W C H L P D P P K K P P -

901 CTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCGGCCAGCA
-----+-----+-----+-----+-----+ 960
GAGAAACCTCCACGCGAGAGACCGTGCGCGGTGAGGGTGGGTAGGCACCCGGCGGTCTGT

a L F G G C A L W H A P L P P I R G P P A -
b S L E G A L S G T R H S H P S V G R Q H -
c L W R V R S L A R A T P T H P W A A S T -

961 CCACGCGGGCCCCCATCCACATCGCGGCCACCACGTCCTGGGACACGCTTGTCCCCG
-----+-----+-----+-----+-----+ 1020
GGTGCGCCCGGGGGTAGGTGTAGCGCCGGTGGTGCAGGACCCTGTGCGGAACAGGGGGC

FIG. 72B



90/103

a P R G P P I H I A A T T S W D T P C P P -
b H A G P P S T S R P P R P G T R L V P R -
c T R A P H P H R G H H V L G H A L S P G -

1021 GTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGNACACTGCGNCCCTC
-----+-----+-----+-----+-----+ 1080
CACATGCGGCTCTGGTTCGTGAAGGAGATGAGGAGTCCGCTGTTCTNTGTGACGCNGGGAG

a V Y A E T K H F L Y S S G D K ? T A ? L -
b C T P R P S T S S T P Q A T ? T L R P S -
c V R R D Q A L P L L L R R Q ? H C ? P P -

1081 CTCCTACTCAATATATCTGAGGCCCGAGCTGACTGGCGTTCGGGAGGTTCTGTGAGACA
-----+-----+-----+-----+-----+ 1140
GAAGGATGAGTTATATAGACTCCGGGTCGACTGACCGCAAGCCCTCCAAGCACCTCTGT

a L P T Q Y I * G P A * L A F G R F V E T -
b F L L N I S E A Q P D W R S G G S W R ? -
c S Y S I Y L R P S L T G V R E V R G D ? -

1141 NTCTTTCTGGTTCAGGCCCTTGATGCCAGGATTCCCCGCAGGTTGCCCCGCTGCCCCA
-----+-----+-----+-----+-----+ 1200
NAGAAAGACCAAGGTCCGGAACCTACGGTCTTAAGGGGCGTCCAACGGGGCGGACGGGGT

a ? F L V P G L G C Q D S P Q V A P P A P -
b S F W F Q A L D A R I P R R L P R L P Q -
c L S G S R P W M P G F P A G C P A C P S -

1201 GCGNTACTGGCAAATGCGGCCCCCTGTTTCTGGAGCTGCTTGGGAACACGCGCAGTGCCC
-----+-----+-----+-----+-----+ 1260
CGCNATGACCGTTTACGCCGGGGACAAAGACCTCGACGAACCCTTGGTGCGCGTCACGGG

a A ? L A N A A P V S G A A W E P R A V P -
b R Y W Q M R P L F L E L L G N H A Q C P -
c ? T G K C G P C F W S C L G T T R S A P -

1261 CTACGGGGTGTTCTCAAGACGCACTGCCCCGTGCGAGCTGCGGTACCCCCAGCAGCCGG
-----+-----+-----+-----+-----+ 1320
GATGCCCCACAAGGAGTTCTGCGTGACGGGCGACGCTCGACGCCAGTGGGGTCGTGCGCC

a L R G V P Q D A L P A A S C G H P S S R -
b Y G V F L K T H C P L R A A V T P A A G -
c T G C S S R R T A R C E L R S P Q Q P V -

1321 TGTCTGTGCCCCGGGAGAAGCCCCAGGGCTCTGTGGCGGGCCCCGAGGAGGAGGAACACAG
-----+-----+-----+-----+-----+ 1380
ACAGACACGGGCCCTCTTCGGGGTCCCAGACACCGCGGGGGCTCCTCCTCTGTGTGTC

a C L C P G E A P G L C G G P R G G G T Q -
b V C A R E K P Q G S V A A P E E E E H R -
c S V P G R S P R A L W R P P R R R N T D -

1381 ACCCCCGTCGCCTGGTGAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTACGGCT
-----+-----+-----+-----+-----+ 1440
TGGGGGCGAGCGGACCACGTCGACGAGGCGGTGCTGTCGTGCGGGACCGTCCACATGCCGA

a T P V A W C S C S A S T A A P G R C T A -
b P P S P G A A A P P A Q Q P L A G V R L -
c P R R L V Q L L R Q H S S P W Q V Y G F -

1441 TCGTGCGGGCCTGCCTGCGCCGGCTGGTGCCCCAGGCCTCTGGGGCTCCAGGCACAACG
-----+-----+-----+-----+-----+ 1500
AGCACGCCCCGACGGACGCGGCCGACCACGGGGGTCCGGAGACCCGAGGTCCGTGTTGC

FIG. 72C



91/103

a S C G P A C A G W C P Q A S G A P G T T -
b R A G L P A P A G A P R P L G L Q A Q R -
c V R A C L R R L V P P G L W G S R H N E -
AACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGAAGCATGCCAAGCTCT
1501 -----+-----+-----+-----+-----+ 1560
TTGCGGCGAAGGAGTCCTTGTGGTTCCTCAAGTAGAGGGACCCCTTCGTACGGTTCGAGA
a N A A S S G T P R S S S P W G S M P S S -
b T P L P Q E H Q E V H L P G E A C Q A L -
c R R F L R N T K K F I S L G K H A K L S -
CGCTGCAGGAGCTGACGTGGAAGATGAGCGTGC GG GACTGCGCTTGGCTGCGCAGGAGCC
1561 -----+-----+-----+-----+-----+ 1620
GCGACGTCCTCGACTGCACCTTCTACTCGCACGCCCTGACGCGAACCGACGCGTCTCGG
a R C R S * R G R * A C G T A L G C A G A -
b A A G A D V E D E R A G L R L A A Q E P -
c L Q E L T W K M S V R D C A W L R R S P -
CAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGT
1621 -----+-----+-----+-----+-----+ 1680
GTCCCCAACCGACACAAGGCCGGCGTCTCGTGGCAGACGCACTCCTCTAGGACCGGTTCA
a Q G L A V F R P Q S T V C V R R S W P S -
b R G W L C S G R R A P S A * G D P G Q V -
c G V G C V P A A E H R L R E E I L A K F -
TCCTGCACTGGCTGATGAGTGTGTACGTGCTGAGCTGCTCAGGTCTTTCTTTTATGTCA
1681 -----+-----+-----+-----+-----+ 1740
AGGACGTGACCGACTACTCACACATGCAGCAGCTCGACGAGTCCAGAAAGAAAATACAGT
a S C T G * * V C T S S S C S G L S F M S -
b P A L A D E C V R R R A A Q V F L L C H -
c L H W L M S V Y V V E L L R S F F Y V T -
CGGAGACCACGTTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAGCAAGT
1741 -----+-----+-----+-----+-----+ 1800
GCCTCTGGTGCAAAGTTTTCTGTCCGAGAAAAAGATGGCCTTCTCACAGACCTCGTTCA
a R R P R F K R T G S F S T G R V S G A S -
b G D H V S K E Q A L F L P E E C L E Q V -
c E T T F Q K N R L F F Y R K S V W S K L -
TGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTGGAAG
1801 -----+-----+-----+-----+-----+ 1860
ACGTTTCGTAACTTAGTCTGTGCTGAACCTTCTCCACGTGACGCCCCTCGACAGCCTTC
a C K A L E S D S T * R G C S C G S C R K -
b A K H W N Q T A L E E G A A A G A V G S -
c Q S I G I R Q H L K R V Q L R E L S E A -
CAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCA
1861 -----+-----+-----+-----+-----+ 1920
GTCTCCAGTCCGTGCTAGCCCTTCGGTCCGGGCGGGACGACTGCAGGTCTGAGGCGAAGT
a Q R S G S I G K P G P P C * R P D S A S -
b R G Q A A S G S Q A R P A D V Q T P L H -
c E V R Q H R E A R P A L L T S R L R F I -
TCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTGCTGGGAGCCAGAA
1921 -----+-----+-----+-----+-----+ 1980
AGGGGTTGCGACTGCCCCGACGCCGGCTAACACTTGTACCTGATGCAGCACCCCTCGGTCTT

FIG. 72D



92/103

a S P S L T G C G R L * T W T T S W E P E -
b P Q A * R A A A D C E H G L R R G S Q N -
c P K P D G L R P I V N M D Y V V G A R T -
CGTTCGCGAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTTCAGCG
1981 -----+-----+-----+-----+-----+ 2040
GCAAGGCGTCTCTTTTCTCCCGGCTCGCAGAGTGGAGCTCCCACTTCCGTGACAAGTCGC
a R S A E K R G P S V S P R G * R H C S A -
b V P Q R K E G R A S H L E G E G T V Q R -
c F R R E K R A E R L T S R V K A L F S V -
TGCTCAACTACGAGCGGGCGGGCGCCCCGGCCTCCTGGGCGCCTCTGTGCTGGGCGCTGG
2041 -----+-----+-----+-----+-----+ 2100
ACGAGTTGATGCTCGCCCGCGCCGCGGGGCGGAGGACCCGCGGAGACACGACCCGGACC
a C S T T S G R G A P A S W A P L C W A W -
b A Q L R A G A A P R P P G R L C A G P G -
c L N Y E R A R R P G L L G A S V L G L D -
ACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCAGGACCCGCCGC
2101 -----+-----+-----+-----+-----+ 2160
TGCTATAGGTGTCCCGGACCGCGTGAAGCACGACGCACACGCCCGGGTCTTGGCGGCG
a T I S T G P G A P S C C V C G P R T R R -
b R Y P Q G L A H L R A A C A G P G P A A -
c D I H R A W R T F V L R V R A Q D P P P -
CTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCCCAGGACA
2161 -----+-----+-----+-----+-----+ 2220
GACTCGACATGAAACAGTTCCACCTACACTGCCCCGCGCATGCTGTGGTAGGGGGTCTGT
a L S C T L S R W M * R A R T T P S P R T -
b * A V L C Q G G C D G R V R H H P P G Q -
c E L Y F V K V D V T G A Y D T I P Q D R -
GGCTCACGGAGGTCATCGCCAGCATCATCAAACCCAGAACACGTACTGCGTGCCTGCGGT
2221 -----+-----+-----+-----+-----+ 2280
CCGAGTGCCTCCAGTAGCGGTCTAGTAGTTTGGGGTCTTGTGCATGACGCACGCAGCCA
a G S R R S S P A S S N P R T R T A C V G -
b A H G G H R Q H H Q T P E H V L R A S V -
c L T E V I A S I I K P Q N T Y C V R R Y -
ATGCCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCCTTCAAGAGCCACGTCT
2281 -----+-----+-----+-----+-----+ 2340
TACGGCACCAGGTCTTCCGGCGGGTACCCGTGCAGGCGTTCGGAAGTTCTCGGTGCAGA
a M P W S R R P P M G T S A R P S R A T S -
b C R G P E G R P W A R P Q G L Q E P R L -
c A V V Q K A A H G H V R K A F K S H V S -
CTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTTCGTGGCTCACCTGCAGGANAACA
2341 -----+-----+-----+-----+-----+ 2400
GATGGAACTGTCTGGAGGTCCGGCATGTACGCTGTCAAGCACCGAGTGGACGTCTNTTGT
a L P * Q T S S R T C D S S W L T C R ? T -
b Y L D R P P A V H A T V R G S P A G ? Q -
c T L T D L Q P Y M R Q F V A H L Q ? N S -
GCCCCGTGAGGGATGCCGTGCTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTG
2401 -----+-----+-----+-----+-----+ 2460
CGGGCGACTCCCTACGGCAGCAGTAGCTCGTCTCGAGGAGGGACTTACTCCGGTCTGCAC

FIG. 72E



93/103

a A R * G M P S S S S R A P P * M R P A V -
b P A E G C R R H R A E L L P E * G Q Q W -
c P L R D A V V I E Q S S S L N E A S S G -

2461 GCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGCAAGT
-----+-----+-----+-----+-----+ 2520
CGGAGAAGCTGCAGAAGGATGCGAAGTACACGGTGGTGCGGCACGCGTAGTCCCCGTTCA

a A S S T S S Y A S C A T T P C A S G A S -
b P L R R L P T L H V P P R R A H Q G Q V -
c L F D V F L R F M C H H A V R I R G K S -

2521 CCTACGTCCAGTGCCAGGGGATCCCCGAGGGCTCCATCCTCTCCACGCTGCTCTGCAGCC
-----+-----+-----+-----+-----+ 2580
GGATGCAGGTACGGTCCCCTAGGGCGTCCCGAGGTAGGAGAGGTGCGACGAGACGTCCGG

a P T S S A R G S R R A P S S P R C S A A -
b L R P V P G D P A G L H P L H A A L Q P -
c Y V Q C Q G I P Q G S I L S T L L C S L -

2581 TGTGCTACGGCGACATGGAGAACAAGCTGTTTGGGGGATTCGGCGGGACGGGCTGCTCC
-----+-----+-----+-----+-----+ 2640
ACACGATGCCGCTGTACCTCTTGTTCGACAAACGCCCTAAGCCGCCCTGCCGACGAGG

a C A T A T W R T S C L R G F G G T G C S -
b V L R R H G E Q A V C G D S A G R A A P -
c C Y G D M E N K L F A G I R R D G L L L -

2641 TGCGTTTGGTGGATGATTTCTTGTGGTGACACCTCACCTCACCCACGCGAAAACCTTCC
-----+-----+-----+-----+-----+ 2700
ACGCAAACCACCTACTAAAGAACAACCACTGTGGAGTGGAGTGGGTGCGCTTTTGAAGG

a C V W W M I S C W * H L T S P T R K P S -
b A F G G * F L V G D T S P H P R E N L P -
c R L V D D F L L V T P H L T H A K T F L -

2701 TCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACCTTGCGGAAGACAG
-----+-----+-----+-----+-----+ 2760
AGTCCTGGGACCAGGCTCCACAGGGACTCATACCGACGCACCACTTGAACGCCTTCTGTG

a S G P W S E V S L S M A A W * T C G R Q -
b Q D P G P R C P * V W L R G E L A E D S -
c R T L V R G V P E Y G C V V N L R K T V -

2761 TGGTGAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGATGCCGG
-----+-----+-----+-----+-----+ 2820
ACCACTTGAAGGGACATCTTCTGCTCCGGGACCCACCGTGCCGAAAAACAAGTCTACGGCC

a W * T S L * K T R P W V A R L L F R C R -
b G E L P C R R R G P G W H G F C S D A G -
c V N F P V E D E A L G G T A F V Q M P A -

2821 CCCACGGCCTATTCCCCTGGTGGCGCCTGCTGCTGGATACCCGGACCCTGGAGGTGCAGA
-----+-----+-----+-----+-----+ 2880
GGGTGCCGGATAAGGGGACCACGCCGGACGACGACCTATGGGCCTGGGACCTCCACGTCT

a P T A Y S P G A A C C W I P G P W R C R -
b P R P I P L V R P A A G Y P D P G G A E -
c H G L F P W C G L L L D T R T L E V Q S -

2881 GCGACTACTCCAGCTATGCCCCGACCTCCATCAGAGCCAGTCTCACCTTCAACCGCGGCT
-----+-----+-----+-----+-----+ 2940
CGCTGATGAGGTGCGATACGGGCCTGGAGGTAGTCTCGGTCAGAGTGAAGTTGGCGCCGA

FIG. 72F



94/103

a A T T P A M P G P P S E P V S P S T A A -
b R L L Q L C P D L H Q S Q S H L Q P R L -
c D Y S S Y A R T S I R A S L T F N R G F -

2941 TCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTGTCACA
-----+-----+-----+-----+-----+ 3000
AGTTCCGACCCTCCTTGTACGCAGCGTTTGAGAAACCCAGAACGCCGACTTCACAGTGT

a S R L G G T C V A N S L G S C G * S V T -
b Q G W E E H A S Q T L W G L A A E V S Q -
c K A G R N M R R K L F G V L R L K C H S -

3001 GCCTGTTTCTGGATTGTGACGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTACAAGA
-----+-----+-----+-----+-----+ 3060
CGGACAAAGACCTAAACGTCCACTTGTGCGAGGTCTGCCACACGTGGTTGTAGATGTTCT

a A C F W I C R * T A S R R C A P T S T R -
b P V S G F A G E Q P P D G V H Q H L Q D -
c L F L D L Q V N S L Q T V C T N I Y K I -

3061 TCCTCCTGCTGCAGGCGTACAGGTTTTCACGCATGTGTGCTGCAGCTCCCATTTCATCAGC
-----+-----+-----+-----+-----+ 3120
AGGAGGACGACGTCCGCATGTCCAAAGTGCGTACACACGACGTGAGGGTAAAGTAGTCG

a S S C C R R T G F T H V C C S S H F I S -
b P P A A G V Q V S R M C A A A P I S S A -
c L L L Q A Y R F H A C V L Q L P F H Q Q -

3121 AAGTTTGAAGAACCCACATTTTCTGCGCGTCATCTCTGACACGGCCTCCCTCTGCT
-----+-----+-----+-----+-----+ 3180
TTCAAACCTTCTTGGGGTGTA AAAAGGACGCGCAGTAGAGACTGTGCCGGAGGGAGACGA

a K F G R T P H F S C A S S L T R P P S A -
b S L E E P H I F P A R H L * H G L P L L -
c V W K N P T F F L R V I S D T A S L C Y -

3181 ACTCCATCCTGAAAGCCAAGAACGCAGGGATGTGCGTGCGGGGCCAAGGGCGCCGCCGCC
-----+-----+-----+-----+-----+ 3240
TGAGGTAGGACTTTCGGTTCCTTGCGTCCCTACAGCGACCCCGGTTCGCCGGCGGCCCGG

a T P S * K P R T Q G C R W G P R A P P A -
b L H P E S Q E R R D V A G G Q G R R R P -
c S I L K A K N A G M S L G A K G A A G P -

3241 CTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCTGCTCAAGCTGACTC
-----+-----+-----+-----+-----+ 3300
GAGACGGGAGGCTCCGGCACGTACCCGACACGGTGGTTCGTAAGGACGAGTTCGACTGAG

a L C P P R P C S G C A T K H S C S S * L -
b S A L R G R A V A V P P S I P A Q A D S -
c L P S E A V Q W L C H Q A F L L K L T R -

3301 GACACCGTGTACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCAGACGCAGCTGA
-----+-----+-----+-----+-----+ 3360
CTGTGGCACAGTGGATGCACGGTGAGGACCCAGTGAGTCTGTGCGGTCTGCGTCGACT

a D T V S P T C H S W G H S G Q P R R S * -
b T P C H L R A T P G V T Q D S P D A A E -
c H R V T Y V P L L G S L R T A Q T Q L S -

3361 GTCGGAAGCTCCCGGGGACGACGTGACTGCCCTGGAGGCCGAGCCAACCCGGCACTGC
-----+-----+-----+-----+-----+ 3420
CAGCCTTCGAGGGCCCTGCTGCGACTGACGGGACCTCCGGCGTCGGTTGGGCCGTGACG

FIG. 72G



95/103

a V G S S R G R R * L P W R P Q P T R H C -
b S E A P G D D A D C P G G R S Q P G T A -
c R K L P G T T L T A L E A A A N P A L P -
CCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCACAGCCAGGCCGAGAGCA
3421 -----+-----+-----+-----+-----+ 3480
GGAGTCTGAAGTTCCTGGTAGGACCTGACTACCGGTGGGCGGGTGTCCGTCCGGCTCTCGT
a P Q T S R P S W T D G H P P T A R P R A -
b L R L Q D H P G L M A T R P Q P G R E Q -
c S D F K T I L D * W P P A H S Q A E S R -
GACACCAGCAGCCCTGTACGCCGGGCTCTACGTCCCAGGGAGGGAGGGGCGGGCCACAC
3481 -----+-----+-----+-----+-----+ 3540
CTGTGGTTCGTCCGGACAGTGGCGCCGAGATGCAGGGTCCCTCCCTCCCCCGCGGGTGTG
a D T S S P V T P G S T S Q G G R G G P H -
b T P A A L S R R A L R P R E G G A A H T -
c H Q Q P C H A G L Y V P G R E G R P T P -
CCAGGCCCGCACCCTGTTGGAGTCTGAGGCCTGAGTGAGTGTGTTGGCCGAGGCCCTGCATGT
3541 -----+-----+-----+-----+-----+ 3600
GGTCCGGGCGTGGCGACCCTCAGACTCCGGACTCACTCACAAACCGGCTCCGGACGTACA
a P G P H R W E S E A * V S V W P R P A C -
b Q A R T A G S L R P E * V F G R G L H V -
c R P A P L G V * G L S E C L A E A C M S -
CCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCTGAGTG
3601 -----+-----+-----+-----+-----+ 3660
GGCCGACTTCCGACTCACAGGCCGACTCCGGACTCGCTCACAGGTCCGTTCCCGACTCAC
a P A E G * V S G * G L S E C P A K G * V -
b R L K A E C P A E A * A S V Q P R A E C -
c G * R L S V R L R P E R V S S Q G L S V -
TCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCACAGGCC
3661 -----+-----+-----+-----+-----+ 3720
AGGTCGTGTGGACGGCAGAAGTGAAGGGGTGTCCGACCGCGAGCCGAGGTGGGGTCCCGG
a S S T P A V F T S P Q A G A R L H P R A -
b P A H L P S S L P H R L A L G S T P G P -
c Q H T C R L H F P T G W R S A P P Q G Q -
AGCTTTTCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCCAGA
3721 -----+-----+-----+-----+-----+ 3780
TCGAAAAGGAGTGGTCTCGGGCCGAAGGTGAGGGGTGTATCCTTATCAGGTAGGGGTCT
a S F S S P G A R L P L P T * E * S I P R -
b A F P H Q E P G F H S P H R N S P S P D -
c L F L T R S P A S T P H I G I V H P Q I -
TTCGCCATTGTTACCCCTCGCCCTGCCCTTTCCTTCCACCCCCACCATCCAGGTG
3781 -----+-----+-----+-----+-----+ 3840
AAGCGGTAACAAGTGGGGAGCGGGACGGGAGGAAACGGAAGGTGGGGGTGGTAGGTCCAC
a F A I V H P S P C P P L P S T P T I Q V -
b S P L F T P R P A L L C L P P P P S R W -
c R H C S P L A L P S F A F H P H H P G G -
GAGACCCTGAGAAGGACCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTGCCCTG
3841 -----+-----+-----+-----+-----+ 3900
CTCTGGGACTCTTCTGGGACCCTCGAGACCCTTAAACCTCACTGGTTTCCACACGGGAC

FIG. 72H

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96/103



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a   E T L R R T L G A L G I W S D Q R C A L -
b   R P * E G P W E L W E F G V T K G V P C -
c   D P E K D P G S S G N L E * P K V C P V -

TACACAGGCGAGGACCCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGGGAGGT
3901 -----+-----+-----+-----+-----+ 3960
ATGTGTCCGCTCCTGGGACGTGGACCTACCCCCAGGGACACCCAGTTTAACCCCCCTCCA

a   Y T G E D P A P G W G S L W V K L G G G -
b   T Q A R T L H L D G G P C G S N W G E V -
c   H R R G P C T W M G V P V G Q I G G R C -

GCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTTGAAAAAAAAAAAAAAAA
3961 -----+-----+-----+-----+-----+ 4020
CGACACCCTCATTTTTATGACTTATATACTCAAAAAGTCAAACTTTTTTTTTTTTTTTTT

a   A V G V K Y * I Y E F F S F E K K K K K -
b   L W E * N T E Y M S F S V L K K K K K K -
c   C G S K I L N I * V F Q F * K K K K K K -

AAAAA
4021 ----- 4029
TTTTTTTTT

a   K K K -
b   K K -
c   K K -

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FIG. 72I

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97/103

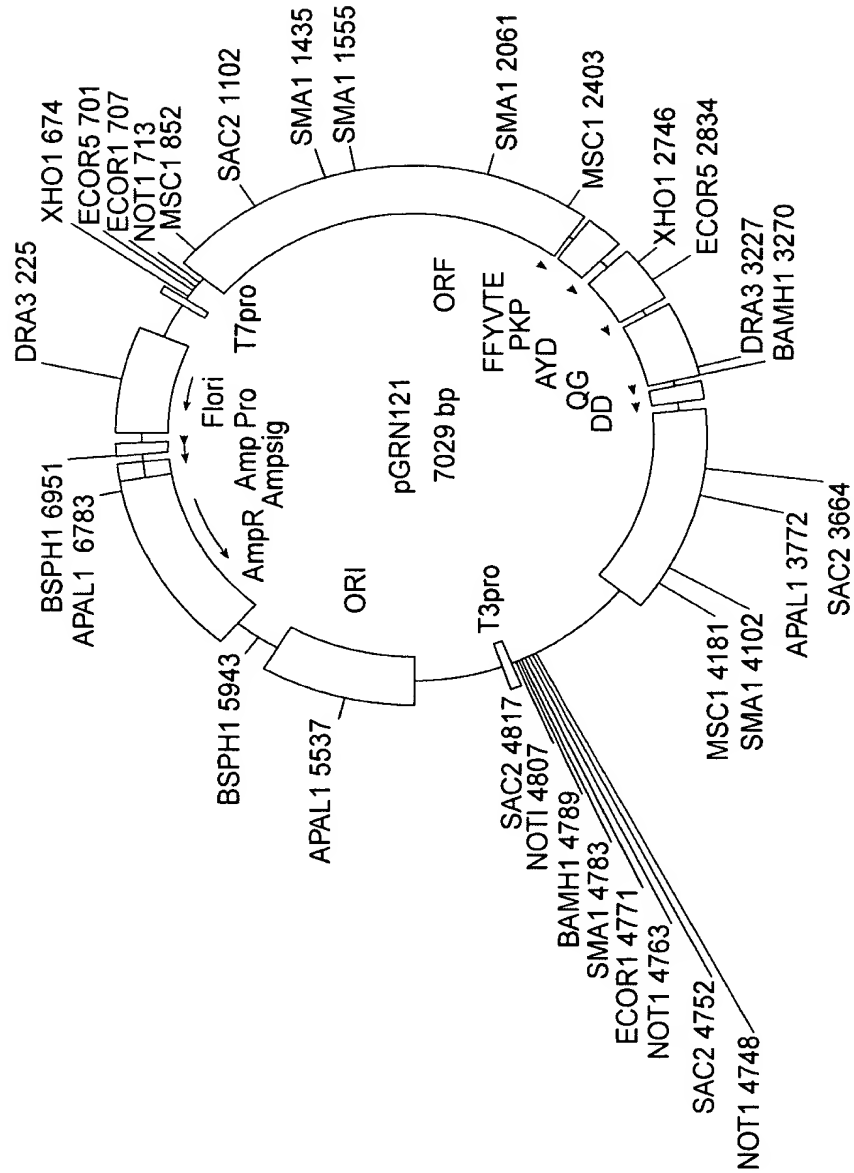


FIG. 73

98/103



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                                                    1
                                                    met
GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCG ATG

                                                    10
pro arg ala pro arg cys arg ala val arg ser leu leu arg ser
CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC

                                                    20
his tyr arg glu val leu pro leu ala thr phe val arg arg leu
CAC TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG

                                                    30
gly pro gln gly trp arg leu val gln arg gly asp pro ala ala
GGG CCC CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT

                                                    40
phe arg ala leu val ala gln cys leu val cys val pro trp asp
TTC CGC GCG CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC

                                                    50
ala arg pro pro pro ala ala pro ser phe arg gln val ser cys
GCA CGG CCG CCC CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC

                                                    60
leu lys glu leu val ala arg val leu gln arg leu cys glu arg
CTG AAG GAG CTG GTG GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC

                                                    70
gly ala lys asn val leu ala phe gly phe ala leu leu asp gly
GGC GCG AAG AAC GTG CTG GCC TTC GGC TTC GCG CTG CTG GAC GGG

                                                    80
ala arg gly gly pro pro glu ala phe thr thr ser val arg ser
GCC CGC GGG GGC CCC CCC GAG GCC TTC ACC ACC AGC GTG CGC AGC

                                                    90
tyr leu pro asn thr val thr asp ala leu arg gly ser gly ala
TAC CTG CCC AAC ACG GTG ACC GAC GCA CTG CGG GGG AGC GGG GCG

                                                    100
trp gly leu leu leu arg arg val gly asp asp val leu val his
TGG GGG CTG CTG CTG CGC CGC GTG GGC GAC GAC GTG CTG GTT CAC

                                                    110
leu leu ala arg cys ala leu phe val leu val ala pro ser cys
CTG CTG GCA CGC TGC GCG CTC TTT GTG CTG GTG GCT CCC AGC TGC

                                                    120
ala tyr gln val cys gly pro pro leu tyr gln leu gly ala ala
GCC TAC CAG GTG TGC GGG CCG CCG CTG TAC CAG CTC GGC GCT GCC

                                                    130
thr gln ala arg pro pro pro his ala ser gly pro arg arg arg
ACT CAG GCC CGG CCC CCG CCA CAC GCT AGT GGA CCC CGA AGG CGT

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FIG. 74A

99/103



												200								210				
leu	gly	cys	glu	arg	ala	trp	asn	his	ser	val	arg	glu	ala	gly										
CTG	GGA	TGC	GAA	CGG	GCC	TGG	AAC	CAT	AGC	GTC	AGG	GAG	GCC	GGG										
												220												
val	pro	leu	gly	leu	pro	ala	pro	gly	ala	arg	arg	arg	gly	gly										
GTC	CCC	CTG	GGC	CTG	CCA	GCC	CCG	GGT	GCG	AGG	AGG	CGC	GGG	GGC										
												230								240				
ser	ala	ser	arg	ser	leu	pro	leu	pro	lys	arg	pro	arg	arg	gly										
AGT	GCC	AGC	CGA	AGT	CTG	CCG	TTG	CCC	AAG	AGG	CCC	AGG	CGT	GGC										
												250												
ala	ala	pro	glu	pro	glu	arg	thr	pro	val	gly	gln	gly	ser	trp										
GCT	GCC	CCT	GAG	CCG	GAG	CGG	ACG	CCC	GTT	GGG	CAG	GGG	TCC	TGG										
												260								270				
ala	his	pro	gly	arg	thr	arg	gly	pro	ser	asp	arg	gly	phe	cys										
GCC	CAC	CCG	GGC	AGG	ACG	CGT	GGA	CCG	AGT	GAC	CGT	GGT	TTC	TGT										
												280												
val	val	ser	pro	ala	arg	pro	ala	glu	glu	ala	thr	ser	leu	glu										
GTG	GTG	TCA	CCT	GCC	AGA	CCC	GCC	GAA	GAA	GCC	ACC	TCT	TTG	GAG										
												290								300				
gly	ala	leu	ser	gly	thr	arg	his	ser	his	pro	ser	val	gly	arg										
GGT	GCG	CTC	TCT	GGC	ACG	CGC	CAC	TCC	CAC	CCA	TCC	GTG	GGC	CGC										
												310												
gln	his	his	ala	gly	pro	pro	ser	thr	ser	arg	pro	pro	arg	pro										
CAG	CAC	CAC	GCG	GGC	CCC	CCA	TCC	ACA	TCG	CGG	CCA	CCA	CGT	CCC										
												320								330				
trp	asp	thr	pro	cys	pro	pro	val	tyr	ala	glu	thr	lys	his	phe										
TGG	GAC	ACG	CCT	TGT	CCC	CCG	GTG	TAC	GCC	GAG	ACC	AAG	CAC	TTC										
												340												
leu	tyr	ser	ser	gly	asp	lys	glu	gln	leu	arg	pro	ser	phe	leu										
CTC	TAC	TCC	TCA	GGC	GAC	AAG	GAG	CAG	CTG	CGG	CCC	TCC	TTC	CTA										
												350								360				
leu	ser	ser	leu	arg	pro	ser	leu	thr	gly	ala	arg	arg	leu	val										
CTC	AGC	TCT	CTG	AGG	CCC	AGC	CTG	ACT	GGC	GCT	CGG	AGG	CTC	GTG										
												370												
glu	thr	ile	phe	leu	gly	ser	arg	pro	trp	met	pro	gly	thr	pro										
GAG	ACC	ATC	TTT	CTG	GGT	TCC	AGG	CCC	TGG	ATG	CCA	GGG	ACT	CCC										
												380								390				
arg	arg	leu	pro	arg	leu	pro	gln	arg	tyr	trp	gln	met	arg	pro										
CGC	AGG	TTG	CCC	CGC	CTG	CCC	CAG	CGC	TAC	TGG	CAA	ATG	CGG	CCC										
												400												
leu	phe	leu	glu	leu	leu	gly	asn	his	ala	gln	cys	pro	tyr	gly										
CTG	TTT	CTG	GAG	CTG	CTT	GGG	AAC	CAC	GCG	CAG	TGC	CCC	TAC	GGG										
												410								420				
val	leu	leu	lys	thr	his	cys	pro	leu	arg	ala	ala	val	thr	pro										
GTG	CTC	CTC	AAG	ACG	CAC	TGC	CCG	CTG	CGA	GCT	GCG	GTC	ACC	CCA										

FIG. 74B

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100/103



430
 ala ala gly val cys ala arg glu lys pro gln gly ser val ala
 GCA GCC GGT GTC TGT GCC CGG GAG AAG CCC CAG GGC TCT GTG GCG

440
 ala pro glu glu glu asp thr asp pro arg arg leu val gln leu
 GCC CCC GAG GAG GAG GAC ACA GAC CCC CGT CGC CTG GTG CAG CTG

460
 leu arg gln his ser ser pro trp gln val tyr gly phe val arg
 CTC CGC CAG CAC AGC AGC CCC TGG CAG GTG TAC GGC TTC GTG CGG

470
 ala cys leu arg arg leu val pro pro gly leu trp gly ser arg
 GCC TGC CTG CGC CGG CTG GTG CCC CCA GGC CTC TGG GGC TCC AGG

490
 his asn glu arg arg phe leu arg asn thr lys lys phe ile ser
 CAC AAC GAA CGC CGC TTC CTC AGG AAC ACC AAG AAG TTC ATC TCC

500
 leu gly lys his ala lys leu ser leu gln glu leu thr trp lys
 CTG GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACG TGG AAG

520
 met ser val arg asp cys ala trp leu arg arg ser pro gly val
 ATG AGC GTG CGG GAC TGC GCT TGG CTG CGC AGG AGC CCA GGG GTT

530
 gly cys val pro ala ala glu his arg leu arg glu glu ile leu
 GGC TGT GTT CCG GCC GCA GAG CAC CGT CTG CGT GAG GAG ATC CTG

550
 ala lys phe leu his trp leu met ser val tyr val val glu leu
 GCC AAG TTC CTG CAC TGG CTG ATG AGT GTG TAC GTC GTC GAG CTG

560
 leu arg ser phe phe tyr val thr glu thr thr phe gln lys asn
 CTC AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC

580
 arg leu phe phe tyr arg pro ser val trp ser lys leu gln ser
 AGG CTC TTT TTC TAC CGG CCG AGT GTC TGG AGC AAG TTG CAA AGC

590
 ile gly ile arg gln his leu lys arg val gln leu arg glu leu
 ATT GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG

610
 ser glu ala glu val arg gln his arg glu ala arg pro ala leu
 TCG GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG

620
 leu thr ser arg leu arg phe ile pro lys pro asp gly leu arg
 CTG ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG

640
 pro ile val asn met asp tyr val val gly ala arg thr phe arg
 CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC

FIG. 74C

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101/103



650
 arg glu lys arg ala glu arg leu thr ser arg val lys ala leu
 AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG

660
 phe ser val leu asn tyr glu arg ala arg arg pro gly leu leu
 TTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC GGC CTC CTG

670
 gly ala ser val leu gly leu asp asp ile his arg ala trp arg
 GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC

680
 thr phe val leu arg val arg ala gln asp pro pro pro glu leu
 ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG CTG

690
 tyr phe val lys val asp val thr gly ala tyr asp thr pro
 TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC

700
 gln asp arg leu thr glu val ile ala ser ile ile lys pro gln
 CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG

710
 asn thr tyr cys val arg arg tyr ala val val gln lys ala ala
 AAC ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC

720
 his gly his val arg lys ala phe lys ser his val ser thr leu
 CAT GGG CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC TCT ACC TTG

730
 thr asp leu gln pro tyr met arg gln phe val ala his leu gln
 ACA GAC CTC CAG CCG TAC ATG CGA CAG TTC GTG GCT CAC CTG CAG

740
 glu thr ser pro leu arg asp ala val val ile glu gln ser ser
 GAG ACC AGC CCG CTG AGG GAT GCC GTC GTC ATC GAG CAG AGC TCC

750
 ser leu asn glu ala ser ser gly leu phe asp val phe leu arg
 TCC CTG AAT GAG GCC AGC AGT GGC CTC TTC GAC GTC TTC CTA CGC

760
 phe met cys his his ala val arg ile arg gly lys ser tyr val
 TTC ATG TGC CAC CAC GCC GTG CGC ATC AGG GGC AAG TCC TAC GTC

770
 gln cys gln gly ile pro gln gly ser ile leu ser thr leu leu
 CAG TGC CAG GGG ATC CCG CAG GGC TCC ATC CTC TCC ACG CTG CTC

780
 cys ser leu cys tyr gly asp met glu asn lys leu phe ala gly
 TGC AGC CTG TGC TAC GGC GAC ATG GAG AAC AAG CTG TTT GCG GGG

790
 ile arg arg asp gly leu leu leu arg leu val asp asp phe leu
 ATT CGG CGG GAC GGG CTG CTC CTG CGT TTG GTG GAT GAT TTC TTG

800
 810
 820
 830
 840
 850
 860
 870

FIG. 74D

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102/103



880
 leu val thr pro his leu thr his ala lys thr phe leu arg thr
 TTG GTG ACA CCT CAC CTC ACC CAC GCG AAA ACC TTC CTC AGG ACC

890
 leu val arg gly val pro glu tyr gly cys val val asn leu arg
 CTG GTC CGA GGT GTC CCT GAG TAT GGC TGC GTG GTG AAC TTG CGG

910
 lys thr val val asn phe pro val glu asp glu ala leu gly gly
 AAG ACA GTG GTG AAC TTC CCT GTA GAA GAC GAG GCC CTG GGT GGC

920
 thr ala phe val gln met pro ala his gly leu phe pro trp cys
 ACG GCT TTT GTT CAG ATG CCG GCC CAC GGC CTA TTC CCC TGG TGC

940
 gly leu leu leu asp thr arg thr leu glu val gln ser asp tyr
 GGC CTG CTG CTG GAT ACC CGG ACC CTG GAG GTG CAG AGC GAC TAC

950
 ser ser tyr ala arg thr ser ile arg ala ser val thr phe asn
 TCC AGC TAT GCC CGG ACC TCC ATC AGA GCC AGT GTC ACC TTC AAC

970
 arg gly phe lys ala gly arg asn met arg arg lys leu phe gly
 CGC GGC TTC AAG GCT GGG AGG AAC ATG CGT CGC AAA CTC TTT GGG

980
 val leu arg leu lys cys his ser leu phe leu asp leu gln val
 GTC TTG CGG CTG AAG TGT CAC AGC CTG TTT CTG GAT TTG CAG GTG

1000
 asn ser leu gln thr val cys thr asn ile tyr lys ile leu leu
 AAC AGC CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG

1010
 leu gln ala tyr arg phe his ala cys val leu gln leu pro phe
 CTG CAG GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT

1030
 his gln gln val trp lys asn pro thr phe phe leu arg val ile
 CAT CAG CAA GTT TGG AAG AAC CCC ACA TTT TTC CTG CGC GTC ATC

1040
 ser asp thr ala ser leu cys tyr ser ile leu lys ala lys asn
 TCT GAC ACG GCC TCC CTC TGC TAC TCC ATC CTG AAA GCC AAG AAC

1060
 ala gly met ser leu gly ala lys gly ala ala gly pro leu pro
 GCA GGG ATG TCG CTG GGG GCC AAG GGC GCC GCC GGC CCT CTG CCC

1070
 ser glu ala val gln trp leu cys his gln ala phe leu leu lys
 TCC GAG GCC GTG CAG TGG CTG TGC CAC CAA GCA TTC CTG CTC AAG

1090
 leu thr arg his arg val thr tyr val pro leu leu gly ser leu
 CTG ACT CGA CAC CGT GTC ACC TAC GTG CCA CTC CTG GGG TCA CTC

FIG. 74E

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103/103



1100 1110
 arg thr ala gln thr gln leu ser arg lys leu pro gly thr thr
 AGG ACA GCC CAG ACG CAG CTG AGT CGG AAG CTC CCG GGG ACG ACG
 1120
 leu thr ala leu glu ala ala ala asn pro ala leu pro ser asp
 CTG ACT GCC CTG GAG GCC GCA GCC AAC CCG GCA CTG CCC TCA GAC
 1130 1132
 phe lys thr ile leu asp OP
 TTC AAG ACC ATC CTG GAC TGA TGGCCACCCGCCCACAGCCAGGCCGAGAGCAGA
 CACCAGCAGCCCTGTACGCCGGGCTCTACGTCCCAGGGAGGGGAGGGGCGGCCACACCC
 AGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTTGGCCGAGGCCTGCATGTCC
 GGCTGAAGGCTGAGTGTCGGGCTGAGGCCTGAGCGAGTGTCAGCCAAGGGCTGAGTGTC
 CAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCAGGGCCAG
 CTTTTCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCCAGATT
 CGCCATTGTTTACCCYTCGCCCTGCCYTCCTTTGCCTTCCACCCCCACCATCCAGGTGGA
 GACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTGCCCTGTA
 CACAGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGGGAGGTGC
 TGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTTGRAAAAAAAAAAAAAAAAAAA
 AAAAAAAAAA

FIG. 74F

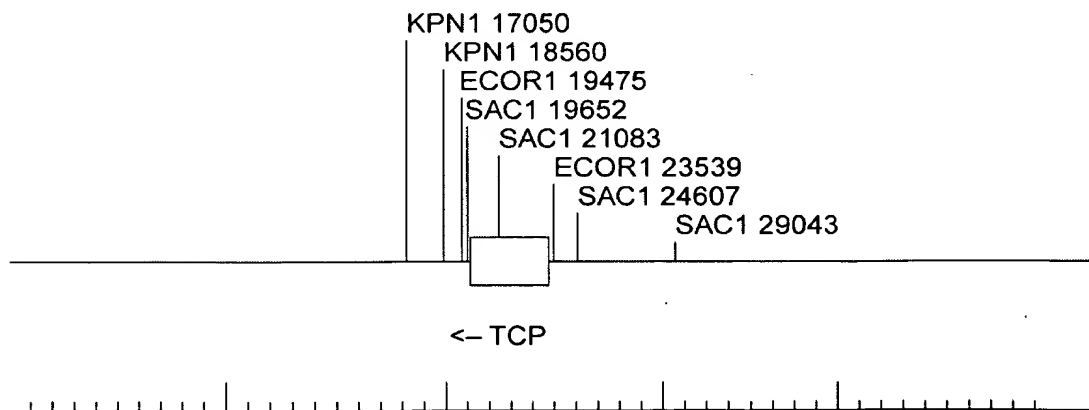


FIG. 75

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